

10/524983

21078WO.ST25.txt  
SEQUENCE LISTING

&lt;110&gt; DSM IP Assets B.V.

&lt;120&gt; NOVEL LIPASES AND USES THEREOF

&lt;130&gt; 21078WO

&lt;160&gt; 39

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 3728

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;400&gt; 1

cgggcaatta	cgtccgagc	gchgctatcta	cgtgcacccgg	aagcttgctc	cttgatttgt	60
tgtttcataa	tacttatttg	tgctctttag	cccgactgca	gtgggtggctg	catgttgggc	120
aggtaattaa	ctttgggcga	taccaactac	gcgtgcactt	tgaagcatag	cacggcgcgc	180
cggggatgcg	tgtcgcttta	tgactataat	tgtatgtggcc	gactgactgc	ttgggtgttag	240
ggatcttgtg	tttatcttgg	ttttctgtac	ttagaagaga	gtgccggtag	catgggtggtc	300
gatataacta	gagcaatgcg	tgtctccatc	ctcatcctca	tcggccatcc	tttataccct	360
gatggcgccg	aagggtgaga	atggcgatgg	gcgagaataa	tataactgtgt	atagtctgtc	420
ctatcctcct	tgtgcactgc	aaagtcagtt	gatcatcatc	cccactcaat	cgtccactca	480
tgtctatat	ccgagacaaa	ccacaactta	ttcaatttaa	gcccggatcc	ataatcatcc	540
acaaccaccc	cacagccagg	gtacatccag	ggtctcttc	ccgccccgaga	aactaagccc	600
ttagctccctc	actaggacct	cccgccgcgt	ttggctcct	catcaccaac	tttccaccta	660
taaactgcat	caaacatgct	gcaaagccac	gactgctgct	gcatgcaccc	caacatcatc	720
cccgataat	acatccatcc	ctgaagcaat	caagcttgcac	tctgttgttt	tttcggagat	780
gttaaccatt	cgtactttcc	aatgacatc	aatccaactg	atagacatcg	ccatcctcct	840
caataccatg	gacgccccac	gtccatgtca	aaagtaagac	tagctcagct	cggcgtaat	900
caattatgtat	tgcgagtctc	aatccctgag	tcatgtgttc	tctgtgtcgg	agaatttagac	960
tgaattcagc	tgctcggtgc	caactcctagc	tccctgataa	aggcctcac	ttcgctcgt	1020
agctggctgg	ctgcatattc	tccggact	aagttAACAG	aaccagcaac	tttagtagcca	1080
tggcgagcgc	actcctctgg	ctctccctgc	tgggtggcag	caccctagcc	tcaactctag	1140
acaccagtaa	taccccttacc	atcaagagag	cagacgcagg	aaacaacacc	tcctcaatcc	1200
caacagccac	cctcaacaac	accgtcttca	tcggccgttc	cctgcccgg	ttcgagcagg	1260
agttgttcct	gggtatcaag	tttgctgatg	ägcccgtgct	attcaccctcg	tcgacgttga	1320
aaaccgtcta	tcgcgccaat	gacagcgaca	acgggggtgta	tcatgcttcc	acagcatccg	1380
gactgcagac	ttcctcgggg	accgtgtct	acaacgcccac	agagtatggg	tatgattgcc	1440
ccgggtatgg	atccgtgag	acggagctgg	cgaggaaagg	atatgcgcgg	ttcgatgaga	1500

## 21078W0.ST25.txt

actgtatgaa cctgaatata attcggccca agagagagaa agaggatgag ttgtgcctg	1560
tgtatgtttt gatcttttgtt ggtgggtggg tgcagggtgc gactgctgat ccgaggtagg	1620
atactatagt ttttgtgtgt gctgtgtggg gtgtatgctg acgtatgtca aggtacaata	1680
tgagctatat tgttcgccag ggtgcgttga atgataagcc tgtcttgggt gtctcgatca	1740
attaccgtgt ggctgcgtt ggattccttgc actctgtcga gttatgggt cgtttcttcc	1800
ttcacccgtca agtatatggg ttcagctga catgacatct gtaggaatcc ggcaacacga	1860
acctaggact tcgtgatcag cgcgtgccca tgcattgggt caaacaacaa atcaaggcgt	1920
ttggtgttga cccggacaag atcaccatct ggggagaatc agcgtgagat tataccctaa	1980
tagcattcga tatacagcgc ctgacatggc acagtggtgc ctacagcgtc ggagccacc	2040
tggtcaccaa cgacgggtac aacgagggtc tattcagagc cggtatgcac accactcccc	2100
aattctcgctc tcctcatctg ctaaccagca tagccatcat ggaatccggc aacgcagtcg	2160
gacccccccta caacggcacg gactggtacc agccgatgtc cgaccagatc gtgaacgcaa	2220
ccaagtatgt cctcaccttc cccaaaagac aatactaaaa tgacttagtat atataactaac	2280
tacatgaaag ctgcaccacc tcaagcaaca cccttcaatg cctccgcgaa gtcccttct	2340
caacgatcta caccggccca gacatcggtt tggaatgggt cgccaccatc gacggcacct	2400
tcatcaaaga atatccccaa atcagcatta cggagggccg cttcgccaa gtcccccattcc	2460
tccatggcac caacaccgac gaggcgtga gtttcgttac gacggcgtg aacactgatg	2520
ccgaagcgat ccacgcgtt atgggtgagc cccccccccc ccccttccc accaatcccc	2580
aagatata tatagtagcga gatactaagg tgaaatgaaa atgatagcat ccaaacgctg	2640
ggtcctaaac gaaacccaag ccacgaccct cctatcgac tatcccaaca tctccgcct	2700
aggctgtccc tacggatggg gcaacacgac ctggccgaag ctgggtatg aatataagcg	2760
ctacgagtcg atggcggcgc atctgtcat gttgtctccg aggaggttc tcagtcagaa	2820
gatgaaggag tatgaggagc aagtgtttgc gtatcggtt gatgtcgctg cgttgaatga	2880
ttcgagtagc attgggttgg cgcattttgc tgaggtatg ccatccatcc atcccattt	2940
attggttttc cctgcgttat gatattttgt atgctaata gttgttactg cgtgcattca	3000
tagatccctt ttgtttcgc caaccctgtg cagaacatca ctccgttggg aagtgtatccc	3060
gcaagactgg agttggtaa tctggccgcg aggtatgtga cggctttgt gacggatttgc	3120
gatccgaatg ggcattgggg tacgttcctc ttctccatct tattagaatt gtgaaatgaa	3180
gcgtgtgggtt ctaatgaggg tgacagtctc tggatcccc cactggccga aatacaacct	3240
cactgatccg agggactttg tggatccgc accgaggat ggaagttatg tggagaagga	3300
tacttttagg acggggggga ttgatttatataatcaatt gtgcgttaag ttgctgctaa	3360
gtagtactac tatatgtata taggagggtg tgggtgaaaa gtagatagta gtactatatc	3420
aaggatggtt agatactata tactatttac tactactgta atgatctat aatcaagact	3480
agaagaaagt ctactgattt gattttcgat gtattgtatc agttgtata	3540
tcaaatcgac aaagagccgc cgtttttatt cattcatatt tcccgccact aagccagtt	3600
actataccat agtagtata taggatccgtt tgatgccgag cagctcaacc tcgctaatttgc	3660
atatcagcat tccaaatccat tttttactg gcaaagaata tttagaagagg aaggaggagg	3720
aggataac	3728

&lt;210&gt; 2

&lt;211&gt; 1749

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

## 21078WO.ST25.txt

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1749)

&lt;400&gt; 2

atg	gct	agc	gca	ctc	ctc	tgg	ctc	tcc	ctg	ctg	ggt	ggc	agc	acc	cta		48
Met	Ala	Ser	Ala	Leu	Leu	Trp	Leu	Ser	Leu	Leu	Gly	Gly	Ser	Thr	Leu		
1	5			10							15						
gcc	tca	act	cta	gac	acc	agt	aat	acc	cct	acc	atc	aag	aga	gca	gac		96
Ala	Ser	Thr	Leu	Asp	Thr	Ser	Asn	Thr	Pro	Thr	Ile	Lys	Arg	Ala	Asp		
	20			25							30						
gca	gga	aac	aac	acc	tcc	tca	atc	cca	aca	gcc	acc	ctc	aac	acc		144	
Ala	Gly	Asn	Asn	Thr	Ser	Ser	Ile	Pro	Thr	Ala	Thr	Leu	Asn	Asn	Thr		
	35			40							45						
gtc	ttc	atc	ggc	cgt	tcc	ctg	ccc	gag	ttc	gag	cag	gag	ttg	ttc	ctg		192
Val	Phe	Ile	Gly	Arg	Ser	Leu	Pro	Glu	Phe	Glu	Gln	Glu	Leu	Phe	Leu		
	50			55							60						
ggt	atc	aag	ttt	gct	gat	gag	ccc	gtg	cga	ttc	acc	ccg	tcg	acg	ttg		240
Gly	Ile	Lys	Phe	Ala	Asp	Glu	Pro	Val	Arg	Phe	Thr	Pro	Ser	Thr	Leu		
	65			70							75			80			
aaa	acc	gtc	tat	cgc	gcc	aat	gac	agc	gac	aac	ggg	gtg	tat	cat	gct		288
Lys	Thr	Val	Tyr	Arg	Ala	Asn	Asp	Ser	Asp	Asn	Gly	Val	Tyr	His	Ala		
	85			90							95						
tcc	aca	gca	tcc	gga	ctg	cag	act	tcc	tcg	ggg	acc	gtg	ctc	tac	aac		336
Ser	Thr	Ala	Ser	Gly	Leu	Gln	Thr	Ser	Ser	Gly	Thr	Val	Leu	Tyr	Asn		
	100			105							110						
gcc	aca	gag	tat	ggg	tat	gat	tgc	ccc	ggg	tat	gga	tcc	gat	gag	acg		384
Ala	Thr	Glu	Tyr	Gly	Tyr	Asp	Cys	Pro	Gly	Tyr	Gly	Ser	Asp	Glu	Thr		
	115			120							125						
gag	ctg	gct	gag	gaa	gga	tat	gct	cgg	ttc	gat	gag	aac	tgt	atg	aac		432
Glu	Leu	Ala	Glu	Glu	Gly	Tyr	Ala	Arg	Phe	Asp	Glu	Asn	Cys	Met	Asn		
	130			135							140						
ctg	aat	ata	att	cg	ccc	aag	aga	gag	aaa	gag	gat	gag	ttg	ttg	cct		480
Leu	Asn	Ile	Ile	Arg	Pro	Lys	Arg	Glu	Lys	Glu	Asp	Glu	Leu	Leu	Pro		
	145			150							155			160			
gtg	atg	att	tgg	atc	ttt	ggt	ggt	tgg	gtg	cag	ggt	gct	act	gct		528	
Val	Met	Ile	Trp	Ile	Phe	Gly	Gly	Trp	Val	Gln	Gly	Ala	Thr	Ala			
	165			170							175						
gat	ccg	agg	tac	aat	atg	agc	tat	att	gtt	cgc	cag	ggt	gct	ttt		576	
Asp	Pro	Arg	Tyr	Asn	Met	Ser	Tyr	Ile	Val	Arg	Gln	Gly	Ala	Leu	Asn		
	180			185							190						
gat	aag	cct	gtc	ttg	ggt	gtc	atc	aat	tac	cgt	gtg	gct	gct	ttt		624	
Asp	Lys	Pro	Val	Leu	Gly	Val	Ser	Ile	Asn	Tyr	Arg	Val	Ala	Ala	Phe		

## 21078WO.ST25.txt

195	200	205	
gga ttc ctt gac tct gtc gag gtt atg gaa tcc ggc aac acg aac cta			672
Gly Phe Leu Asp Ser Val Glu Val Met Glu Ser Gly Asn Thr Asn Leu			
210	215	220	
gga ctt cgt gat cag cgc gtc gcc atg cat tgg gtc aaa caa aac atc			720
Gly Leu Arg Asp Gln Arg Val Ala Met His Trp Val Lys Gln Asn Ile			
225	230	235	240
aag gcg ttt ggt ggt gac ccg gac aag atc acc atc tgg gga gaa tca			768
Lys Ala Phe Gly Gly Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser			
245	250	255	
gct ggt gcc tac agc gtc gga gcc cac ctg gtc acc aac gac ggt gac			816
Ala Gly Ala Tyr Ser Val Gly Ala His Leu Val Thr Asn Asp Gly Asp			
260	265	270	
aac gag ggt cta ttc aga gcc gcc atc atg gaa tcc ggc aac gca gtc			864
Asn Glu Gly Leu Phe Arg Ala Ala Ile Met Glu Ser Gly Asn Ala Val			
275	280	285	
gga ccc ccc tac aac ggc acg gac tgg tac cag ccg atg tac gac cag			912
Gly Pro Pro Tyr Asn Gln Thr Asp Trp Tyr Gln Pro Met Tyr Asp Gln			
290	295	300	
atc gtg aac gca acc aac tgc acc acc tca acg aac acc ctt caa tgc			960
Ile Val Asn Ala Thr Asn Cys Thr Thr Ser Ser Asn Thr Leu Gln Cys			
305	310	315	320
ctc cgc gaa gtc ccc ttc tca acg atc tac acc gcc gca gac atc ggc			1008
Leu Arg Glu Val Pro Phe Ser Thr Ile Tyr Thr Ala Ala Asp Ile Gly			
325	330	335	
ctg gaa tgg ttc gcc acc atc gac ggc acc ttc atc aaa gaa tat ccc			1056
Leu Glu Trp Phe Ala Thr Ile Asp Gly Thr Phe Ile Lys Glu Tyr Pro			
340	345	350	
caa atc acg att acg gag ggc cgc ttc gcc aag gtc ccc atc ctc cat			1104
Gln Ile Ser Ile Thr Glu Gly Arg Phe Ala Lys Val Pro Ile Leu His			
355	360	365	
ggc acc aac acc gac gag ggc gtg agt ttc ggt acg acg ggc gtg aac			1152
Gly Thr Asn Thr Asp Glu Gly Val Ser Phe Gly Thr Thr Gly Val Asn			
370	375	380	
act gat gcc gaa gcg atc cag cag ttg atg gca tcc aaa cgc tgg gtc			1200
Thr Asp Ala Glu Ala Ile Gln Gln Leu Met Ala Ser Lys Arg Trp Val			
385	390	395	400
cta aac gaa acc caa gcc acg acc ctc cta tcg cac tat ccc aac atc			1248
Leu Asn Glu Thr Gln Ala Thr Thr Leu Leu Ser His Tyr Pro Asn Ile			
405	410	415	
tcc gcc cta ggc tgt ccc tac gga tgg ggc aac acg acc tgg ccg aag			1296
Ser Ala Leu Gly Cys Pro Tyr Gly Trp Gly Asn Thr Thr Trp Pro Lys			
420	425	430	
ctg ggg tat gaa tat aag cgc tac gag tcg atg gcg ggc gat ctg tgc			1344

## 21078WO.ST25.txt

Leu Gly Tyr Glu Tyr Lys Arg Tyr Glu Ser Met Ala G1y Asp Leu Cys			
435	440	445	
atg gtt gct ccg agg agg ttg ctc agt cag aag atg aag gag tat gag			1392
Met Val Ala Pro Arg Arg Leu Leu Ser Gln Lys Met Lys Glu Tyr Glu			
450	455	460	
gag caa gtg ttt gcg tat cgg tgg gat gtc gct gcg ttg aat gat tcg			1440
Glu Gln Val Phe Ala Tyr Arg Trp Asp Val Ala Ala Leu Asn Asp Ser			
465	470	475	480
agt acg att ggg gtg gcg cat ttt gct gag atc ccg ttt gtt ttc gcc			1488
Ser Thr Ile Gly Val Ala His Phe Ala Glu Ile Pro Phe Val Phe Ala			
485	490	495	
aac cct gtg cag aac atc act ccg ttg gga agt gat ccc gca aga ctg			1536
Asn Pro Val Gln Asn Ile Thr Pro Leu Gly Ser Asp Pro Ala Arg Leu			
500	505	510	
gag ttg ggt aat ctg gcc gcg agg atg tgg acg gct ttt gtg acg gat			1584
Glu Leu Gly Asn Leu Ala Ala Arg Met Trp Thr Ala Phe Val Thr Asp			
515	520	525	
ttg gat ccg aat ggg cat ggt gtc tct ggt atc ccc cac tgg ccg aaa			1632
Leu Asp Pro Asn Gly His Gly Val Ser Gly Ile Pro His Trp Pro Lys			
530	535	540	
tac aac ctc act gat ccg agg gac ttt gtg ttc ccg cta ccg agg gat			1680
Tyr Asn Leu Thr Asp Pro Arg Asp Phe Val Phe Arg Leu Pro Arg Asp			
545	550	555	560
gga agt tat gtg gag aag gat act ttt agg acg ggg ggg att gat tat			1728
Gly Ser Tyr Val Glu Lys Asp Thr Phe Arg Thr Gly Gly Ile Asp Tyr			
565	570	575	
att aat aca att gtg ccg taa			1749
Ile Asn Thr Ile Val Arg			
580			

&lt;210&gt; 3

&lt;211&gt; 582

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 3

Met Ala Ser Ala Leu Leu Trp Leu Ser Leu Leu G1y G1y Ser Thr Leu			
1	5	10	15
Ala Ser Thr Leu Asp Thr Ser Asn Thr Pro Thr Ile Lys Arg Ala Asp			
20	25	30	
Ala G1y Asn Asn Thr Ser Ser Ile Pro Thr Ala Thr Leu Asn Asn Thr			
35	40	45	
Val Phe Ile G1y Arg Ser Leu Pro Glu Phe Glu Gln Glu Leu Phe Leu			

## 21078WO.ST25.txt

50	55	60
Gly Ile Lys Phe Ala Asp Glu Pro Val Arg Phe Thr Pro Ser Thr Leu		
65	70	75
Lys Thr Val Tyr Arg Ala Asn Asp Ser Asp Asn Gly Val Tyr His Ala		80
85	90	95
Ser Thr Ala Ser Gly Leu Gln Thr Ser Ser Gly Thr Val Leu Tyr Asn		
100	105	110
Ala Thr Glu Tyr Gly Tyr Asp Cys Pro Gly Tyr Gly Ser Asp Glu Thr		
115	120	125
Glu Leu Ala Glu Glu Gly Tyr Ala Arg Phe Asp Glu Asn Cys Met Asn		
130	135	140
Leu Asn Ile Ile Arg Pro Lys Arg Glu Lys Glu Asp Glu Leu Leu Pro		
145	150	155
Val Met Ile Trp Ile Phe Gly Gly Trp Val Gln Gly Ala Thr Ala		160
165	170	175
Asp Pro Arg Tyr Asn Met Ser Tyr Ile Val Arg Gln Gly Ala Leu Asn		
180	185	190
Asp Lys Pro Val Leu Gly Val Ser Ile Asn Tyr Arg Val Ala Ala Phe		
195	200	205
Gly Phe Leu Asp Ser Val Glu Val Met Glu Ser Gly Asn Thr Asn Leu		
210	215	220
Gly Leu Arg Asp Gln Arg Val Ala Met His Trp Val Lys Gln Asn Ile		
225	230	235
Lys Ala Phe Gly Gly Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser		240
245	250	255
Ala Gly Ala Tyr Ser Val Gly Ala His Leu Val Thr Asn Asp Gly Asp		
260	265	270
Asn Glu Gly Leu Phe Arg Ala Ala Ile Met Glu Ser Gly Asn Ala Val		
275	280	285
Gly Pro Pro Tyr Asn Gly Thr Asp Trp Tyr Gln Pro Met Tyr Asp Gln		
290	295	300
Ile Val Asn Ala Thr Asn Cys Thr Thr Ser Ser Asn Thr Leu Gln Cys		
305	310	315
Leu Arg Glu Val Pro Phe Ser Thr Ile Tyr Thr Ala Ala Asp Ile Gly		320
325	330	335
Leu Glu Trp Phe Ala Thr Ile Asp Gly Thr Phe Ile Lys Glu Tyr Pro		
340	345	350
Gln Ile Ser Ile Thr Glu Gly Arg Phe Ala Lys Val Pro Ile Leu His		
355	360	365
Gly Thr Asn Thr Asp Glu Gly Val Ser Phe Gly Thr Thr Gly Val Asn		
370	375	380
Thr Asp Ala Glu Ala Ile Gln Gln Leu Met Ala Ser Lys Arg Trp Val		
385	390	395
Leu Asn Glu Thr Gln Ala Thr Thr Leu Leu Ser His Tyr Pro Asn Ile		400

## 21078WO.ST25.txt

405	410	415
Ser Ala Leu Gly Cys Pro Tyr Gly Trp Gly Asn Thr Thr Trp Pro Lys		
420	425	430
Leu Gly Tyr Glu Tyr Lys Arg Tyr Glu Ser Met Ala Gly Asp Leu Cys		
435	440	445
Met Val Ala Pro Arg Arg Leu Leu Ser Gln Lys Met Lys Glu Tyr Glu		
450	455	460
Glu Gln Val Phe Ala Tyr Arg Trp Asp Val Ala Ala Leu Asn Asp Ser		
465	470	475
480		
Ser Thr Ile Gly Val Ala His Phe Ala Glu Ile Pro Phe Val Phe Ala		
485	490	495
Asn Pro Val Gln Asn Ile Thr Pro Leu Gly Ser Asp Pro Ala Arg Leu		
500	505	510
Glu Leu Gly Asn Leu Ala Ala Arg Met Trp Thr Ala Phe Val Thr Asp		
515	520	525
Leu Asp Pro Asn Gly His Gly Val Ser Gly Ile Pro His Trp Pro Lys		
530	535	540
Tyr Asn Leu Thr Asp Pro Arg Asp Phe Val Phe Arg Leu Pro Arg Asp		
545	550	555
560		
Gly Ser Tyr Val Glu Lys Asp Thr Phe Arg Thr Gly Gly Ile Asp Tyr		
565	570	575
Ile Asn Thr Ile Val Arg		
580		

&lt;210&gt; 4

&lt;211&gt; 3853

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;400&gt; 4

ctttcctgtt gcccgtctt tggtgtgtc ataggataca attacccaga caacgttcgg	60
tttgtcgatc agtttaagt gtgcgtggac tgacagccaa ggccactggg gccccctgcct	120
ctatcattta attcccacacg ctcgcctctg cagctctggc accagcgttg caaattccag	180
gggtcagcct acgtggcatt aggctctaag agaatctgag gcaaaggatt tcacttagaa	240
aaatttatcg gtccggcttg tccgatcggt aggaaggcat tgcttccct catatgcggc	300
cccggttccc aagcagctga ttccggacgt tttccggctt gatcgctata ctctcataat	360
ctctcctgca agagctggat aaacttggtt tcttatcttc cgtggggatg ccatagtcca	420
gtagacgctg tctcgaaatt gagtagcacc actattacg gcaagttaa tggcacatgt	480
attagcttg tactgacggt tgaaatgtgg agcaatttcc ggctatgtac cgatctgtt	540
ccggatatct tcatcgcaat tagtttagtac ataaaactcc ctagtcacgc aagaacggtt	600
cgaacataac gaattaaaaaa ttctcattct ctggcaaggc ttgaaatgtt ttgtttcctc	660
gcttgctcta ttagcactta ttgctcctt gatcgcaatt gcgttaaaaa tagaacagcc	720
aggaataaat ccaaataccca cagctactgt acgaaatggc acctactatg gtctccataa	780

## 21078WO.ST25.txt

ccagcactat	aatcaagacc	tctttctcg	tattccatat	gcacagcaac	ctattggta	840
ccttcgctt	cgaccccac	gatcaatgaa	cacccctcg	ccagtagcaa	gaaatgcaac	900
agaatattca	ccccatgtg	ttggatttaa	tcagacagag	ggtgcttcc	aaggctgcct	960
tactctcaat	gtcgccg	cgcaagcat	cgctttct	gaaagtctc	ccgttgctgg	1020
tcagtatata	ccccaaatct	gatcagaagg	gccagaactg	acttgcgt	cggcccccagt	1080
ctggattcat	ggcggggat	tcaccccg	ctcttcatca	gagaaacaat	acaatctgtc	1140
cttcatcg	gatcagtca	tccaaatgga	aaagccgtt	atcgagtc	gtctaaatta	1200
tcgtcttcaa	tgctgggtt	ttatgtggag	caaggagatg	aaggaagccg	gagtagggaa	1260
cctggactt	agagaccaac	gattagctc	gcattggata	caagaaagta	ggtatctcg	1320
tagtgaagct	cttccaagta	cggatctgac	catgacttag	acattgctgc	gtttgggtgg	1380
gaccctgctc	agttacaat	ttggggtgaa	agtgcggcg	ctaatagtgt	tggcacacat	1440
ctggttgctt	acggaggcg	cgatgatgt	atattccgt	cagctatcag	tgaaagtgg	1500
gccccaaatg	tttaccaacg	ttatccaaca	cctgctgaat	ggcagcccta	ttatgtatgg	1560
attgtgaatg	catcaggctg	cagttcagca	acggatactt	tggcttgtct	ccgaacaatt	1620
ccaactaaca	tattgcatgg	catcttgcac	aacacgtcta	ttgtacccat	gcacgctatt	1680
tcaggcctca	gcccggcaaa	attcattcct	gtcatagatg	acgacttcat	taaagagagt	1740
gccacggttc	agctccagaa	ggcaacttc	gtcaaagttc	cctacttgat	tggagcta	1800
gccgacgaag	ggactgcatt	tgctgtggag	ggagtcaaca	cagatgctga	gtttcgcgag	1860
ctagtcaaag	gttggggcct	caacaacgct	accacggata	tcttgaggc	cctataccca	1920
gacattcctc	agataggaat	ccccggcata	atgggtggaa	ggccaccgtc	cggatatgg	1980
aatcaataca	agcgtgtggc	cgcatittcag	ggtgatgtt	acatccatgc	cgcacgtagg	2040
ttgaccagtc	agatctggc	atcccgcaat	atctcagtt	atagctacat	gtttgacg	2100
atcagccctg	gatatggccc	ctctgctgt	tcctatgctg	ggctactca	tggactgt	2160
attccgtacg	ttttctataa	tctggatggc	ctggggat	actcgaacaa	caagtccata	2220
gaaagcatac	ctaacagtt	ttcccgcatg	agcaaaaat	tgtcaagaat	gtgggtcag	2280
tttgtgacaa	cattggaccc	aaatcattt	ggaggtatgg	tcccacatcc	cattcctat	2340
attgcgcata	gtcagacccg	agctgaatca	actatctt	taggaactaa	tgttcagtg	2400
ccgccccata	atatcgataa	tccggagata	atcttttcg	ataccgatgt	cacgaaccc	2460
acatatgtga	gttctgacgt	ttaccgtcg	gagggcataa	aatacatcg	tgatcacctt	2520
gcaagtgatt	tcgggcactg	agatcacata	tcttctcg	ctaatttt	aatgactgt	2580
gtctcatcta	accagactt	gcccgacgt	ctttacgccc	actgggtgt	attgatgca	2640
cccccaagct	atatagtgtc	tggggttt	aactactgtc	aatgagcga	aattgactat	2700
ttccctt	gactcatgt	gtacgattt	tgctggact	gtgatcaaga	tatgtttt	2760
gagattaccg	gtacgaggt	agtcgtatgc	gccaatatt	ttcatctata	atgaatagta	2820
ataacttagg	agtcattcag	tatagtgc	actgacataa	gtatctt	ttgtatatt	2880
tataatatgt	cccggttggc	cttgggtt	gtactctca	tagcctgct	cttgagaact	2940
catctgttca	atcatagaga	taccaattat	ggaaggatag	gttggcatcg	gtgtttgtt	3000
catcaagact	actaccta	aagtcaactg	agaaggctgt	agactgaaag	cgcgacatt	3060
atgatttagaa	ttccaactt	ggtcaacata	tgcattagac	tataaaagg	acatgttaga	3120
agaactaagt	acatacgacc	atagggtgt	gaaaacagg	cttcccgtcc	gctcagccgt	3180
acttaagcca	cacgcccgg	ggttagt	tgggtgggt	accaccagcg	aatccctt	3240
gttgtatgtt	tttgtttctc	tataaaactt	ttggtcggc	atctcgagat	gtcttccagg	3300
atgctaaaac	cttcgggttc	ctcacagcg	agatgggt	aactggctt	ttaatgtcat	3360
tcttggtt	agtgcgt	aacacggca	tatagtacga	tgatatctga	agtttgggt	3420

## 21078WO.ST25.txt

gtcaagacat atgcttattg tgaccaccag accataaaatc ggagtattca cagcttatat	3480
catcctcaaa cattgattgc atagtagagt gtctaactct tgactcaagg gattgaaaat	3540
gattatttga aaatataggt agtttgaat aacattctgg cacacgagct ttagctggat	3600
tagtaagatg tgacgccat tttgggttg attatgtcat catttggcag ttcccccaga	3660
ggacagcccg gttaagaacg aacctttct gagccgtat acaaatgcgg ggaacagaga	3720
tgaggagatg ccgaagcatg ctttggcaaa cagaagccac tgtaaaaaac cattcacaga	3780
tatcttgtga tagtggatt gcactgactg tccgcgaaag cgagcatatc tatcccgtat	3840
actgagaact agt	3853

&lt;210&gt; 5

&lt;211&gt; 1743

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1743)

&lt;400&gt; 5

atg ttt gtt tcc tcg ctt gct cta tta gca ctt att gct cct ttg atc	48
Met Phe Val Ser Ser Leu Ala Leu Leu Ala Leu Ile Ala Pro Leu Ile	
1 5 10 15	
gca att gcg gta aaa ata gaa cag cca gga ata aat cca aat ccc aca	96
Ala Ile Ala Val Lys Ile Glu Gln Pro Gly Ile Asn Pro Asn Pro Thr	
20 25 30	
gct act gta cga aat ggc acc tac tat ggt ctc cat aac cag cac tat	144
Ala Thr Val Arg Asn Gly Thr Tyr Gly Leu His Asn Gln His Tyr	
35 40 45	
aat caa gac ctc ttt ctc ggt att cca tat gca cag caa cct att ggt	192
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Gln Pro Ile Gly	
50 55 60	
gac ctt cgc ttg cgg acc cca cga tca atg aac acc tcc tgg cca gta	240
Asp Leu Arg Leu Arg Thr Pro Arg Ser Met Asn Thr Ser Trp Pro Val	
65 70 75 80	
cca aga aat gca aca gaa tat tca ccc gca tgt gtt gga ttt aat cag	288
Pro Arg Asn Ala Thr Glu Tyr Ser Pro Ala Cys Val Gly Phe Asn Gln	
85 90 95	
aca gag ggt gct tcc gaa gcc tgc ctt act ctc aat gtc gtc cgc ccg	336
Thr Glu Gly Ala Ser Glu Ala Cys Leu Thr Leu Asn Val Val Arg Pro	
100 105 110	
gca agc atc gct ctt tct gaa agt ctt ccc gtt gct gtc tgg att cat	384
Ala Ser Ile Ala Leu Ser Glu Ser Leu Pro Val Ala Val Trp Ile His	
115 120 125	

## 21078WO.ST25.txt

ggc ggg gga ttc acc tcc ggc tct tca tca gag aaa caa tac aat ctg Gly Gly Gly Phe Thr Ser Gly Ser Ser Glu Lys Gln Tyr Asn Leu 130 135 140	432
tcc ttc atc gtt gat cag tca gtc caa atg gaa aag ccc gtt atc gca Ser Phe Ile Val Asp Gln Ser Val Gln Met Glu Lys Pro Val Ile Ala 145 150 155 160	480
gtc agt cta aat tat cgt ctt caa tgc tgg ggt ttt atg tgg agc aag Val Ser Leu Asn Tyr Arg Leu Gln Cys Trp Gly Phe Met Trp Ser Lys 165 170 175	528
gag atg aag gaa gcc gga gta ggg aac ctg gga ctt aga gac caa cga Glu Met Lys Glu Ala Gly Val Gly Asn Leu Gly Leu Arg Asp Gln Arg 180 185 190	576
tta gct ctg cat tgg ata caa gaa aac att gct gcg ttt ggt gga gac Leu Ala Leu His Trp Ile Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp 195 200 205	624
cct gct cag gtt aca att tgg ggt gaa agt gcc ggc gct aat agt gtt Pro Ala Gln Val Thr Ile Trp Gly Glu Ser Ala Gly Ala Asn Ser Val 210 215 220	672
ggc aca cat ctg gtt gct tac gga ggg cgc gat gat ggt ata ttc cgt Gly Thr His Leu Val Ala Tyr Gly Gly Arg Asp Asp Gly Ile Phe Arg 225 230 235 240	720
gca gct atc agt gaa agt ggt gcc cca agt gtt tac caa cgt tat cca Ala Ala Ile Ser Glu Ser Gly Ala Pro Ser Val Tyr Gln Arg Tyr Pro 245 250 255	768
aca cct gct gaa tgg cag ccc tat tat gat ggt att gtg aat gca tca Thr Pro Ala Glu Trp Gln Pro Tyr Tyr Asp Gly Ile Val Asn Ala Ser 260 265 270	816
ggc tgc agt tca gca acg gat act ttg gct tgt ctc cga aca att cca Gly Cys Ser Ser Ala Thr Asp Thr Leu Ala Cys Leu Arg Thr Ile Pro 275 280 285	864
act aac ata ttg cat ggc atc ttt gac aac acg tct att gta ccc atg Thr Asn Ile Leu His Gly Ile Phe Asp Asn Thr Ser Ile Val Pro Met 290 295 300	912
cac gct att tca ggc ctc agc gga gca aaa ttc att cct gtc ata gat His Ala Ile Ser Gly Leu Ser Gly Ala Lys Phe Ile Pro Val Ile Asp 305 310 315 320	960
gac gac ttc att aaa gag agt gcc acg gtt cag ctc cag aag ggc aac Asp Asp Phe Ile Lys Glu Ser Ala Thr Val Gln Leu Gln Lys Gly Asn 325 330 335	1008
ttc gtc aaa gtt ccc tac ttg att gga gct aac gcc gac gaa ggg act Phe Val Lys Val Pro Tyr Leu Ile Gly Ala Asn Ala Asp Glu Gly Thr 340 345 350	1056
gca ttt gct gtg gag gga gtc aac aca gat gct gag ttt cgc gag cta Ala Phe Ala Val Glu Gly Val Asn Thr Asp Ala Glu Phe Arg Glu Leu	1104

## 21078WO.ST25.txt

355	360	365	
gtc aaa ggt tgg ggc ctc aac aac gct acc acg gat atc ttg gag gcc			1152
Val Lys Gly Trp Gly Leu Asn Asn Ala Thr Thr Asp Ile Leu Glu Ala			
370	375	380	
cta tac cca gac att cct cag ata gga atc ccc gcc ata atg gtt gga			1200
Leu Tyr Pro Asp Ile Pro Gln Ile Gly Ile Pro Ala Ile Met Val Gly			
385	390	395	400
agg cca ccg tcc gga tat gga aat caa tac aag cgt gtg gcc gca ttt			1248
Arg Pro Pro Ser Gly Tyr Gly Asn Gln Tyr Lys Arg Val Ala Ala Phe			
405	410	415	
cag ggt gat gtt aac atc cat gcc gca cgt agg ttg acc agt cag atc			1296
Gln Gly Asp Val Asn Ile His Ala Ala Arg Arg Leu Thr Ser Gln Ile			
420	425	430	
tgg tca tcc cgc aat atc tca gta tat agc tac atg ttt gac gtt atc			1344
Trp Ser Ser Arg Asn Ile Ser Val Tyr Ser Tyr Met Phe Asp Val Ile			
435	440	445	
agc cct gga tat ggc ccc tct gct ggt tcc tat gct ggg gct act cat			1392
Ser Pro Gly Tyr Gly Pro Ser Ala Gly Ser Tyr Ala Gly Ala Thr His			
450	455	460	
ggt act gat att ccg tac gtt ttc tat aat ctg gat ggc ctg ggg tat			1440
Gly Thr Asp Ile Pro Tyr Val Phe Tyr Asn Leu Asp Gly Leu Gly Tyr			
465	470	475	480
gac tcg aac aac aag tcc ata gaa agc ata cct aac agt tat tcc cgc			1488
Asp Ser Asn Asn Lys Ser Ile Glu Ser Ile Pro Asn Ser Tyr Ser Arg			
485	490	495	
atg agc aaa att atg tca aga atg tgg gtc agt ttt gtg aca aca ttg			1536
Met Ser Lys Ile Met Ser Arg Met Trp Val Ser Phe Val Thr Thr Leu			
500	505	510	
gac cca aat cat tct gga ggt atg gtc cca cat ccc att cct atg att			1584
Asp Pro Asn His Ser Gly Gly Met Val Pro His Pro Ile Pro Met Ile			
515	520	525	
gcg caa tgt cag acc cga gct gaa tca act atc ttc tta gga act aat			1632
Ala Gln Cys Gln Thr Arg Ala Glu Ser Thr Ile Phe Leu Gly Thr Asn			
530	535	540	
gtt cag tgg ccg cca tac aat atc gat aat ccg gag ata atc ttt ttc			1680
Val Gln Trp Pro Pro Tyr Asn Ile Asp Asn Pro Glu Ile Ile Phe Phe			
545	550	555	560
gat acc gat gtc acg aac ctc aca tat act tgg ccc gca ggt ctt tac			1728
Asp Thr Asp Val Thr Asn Leu Thr Tyr Thr Trp Pro Ala Gly Leu Tyr			
565	570	575	
gcc cac tgg tgg taa			1743
Ala His Trp Trp			
580			

## 21078WO.ST25.txt

&lt;210&gt; 6

&lt;211&gt; 580

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 6

Met Phe Val Ser Ser Leu Ala Leu Leu Ala Leu Ile Ala Pro Leu Ile  
1 5 10 15  
Ala Ile Ala Val Lys Ile Glu Gln Pro Gly Ile Asn Pro Asn Pro Thr  
20 25 30  
Ala Thr Val Arg Asn Gly Thr Tyr Tyr Gly Leu His Asn Gln His Tyr  
35 40 45  
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Gln Pro Ile Gly  
50 55 60  
Asp Leu Arg Leu Arg Thr Pro Arg Ser Met Asn Thr Ser Trp Pro Val  
65 70 75 80  
Pro Arg Asn Ala Thr Glu Tyr Ser Pro Ala Cys Val Gly Phe Asn Gln  
85 90 95  
Thr Glu Gly Ala Ser Glu Ala Cys Leu Thr Leu Asn Val Val Arg Pro  
100 105 110  
Ala Ser Ile Ala Leu Ser Glu Ser Leu Pro Val Ala Val Trp Ile His  
115 120 125  
Gly Gly Phe Thr Ser Gly Ser Ser Ser Glu Lys Gln Tyr Asn Leu  
130 135 140  
Ser Phe Ile Val Asp Gln Ser Val Gln Met Glu Lys Pro Val Ile Ala  
145 150 155 160  
Val Ser Leu Asn Tyr Arg Leu Gln Cys Trp Gly Phe Met Trp Ser Lys  
165 170 175  
Glu Met Lys Glu Ala Gly Val Gly Asn Leu Gly Leu Arg Asp Gln Arg  
180 185 190  
Leu Ala Leu His Trp Ile Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp  
195 200 205  
Pro Ala Gln Val Thr Ile Trp Gly Glu Ser Ala Gly Ala Asn Ser Val  
210 215 220  
Gly Thr His Leu Val Ala Tyr Gly Gly Arg Asp Asp Gly Ile Phe Arg  
225 230 235 240  
Ala Ala Ile Ser Glu Ser Gly Ala Pro Ser Val Tyr Gln Arg Tyr Pro  
245 250 255  
Thr Pro Ala Glu Trp Gln Pro Tyr Tyr Asp Gly Ile Val Asn Ala Ser  
260 265 270  
Gly Cys Ser Ser Ala Thr Asp Thr Leu Ala Cys Leu Arg Thr Ile Pro  
275 280 285  
Thr Asn Ile Leu His Gly Ile Phe Asp Asn Thr Ser Ile Val Pro Met

## 21078WO.ST25.txt

290	295	300
His Ala Ile Ser Gly Leu Ser Gly Ala Lys Phe Ile Pro Val Ile Asp		
305	310	315
Asp Asp Phe Ile Lys Glu Ser Ala Thr Val Gln Leu Gln Lys Gly Asn		
325	330	335
Phe Val Lys Val Pro Tyr Leu Ile Gly Ala Asn Ala Asp Glu Gly Thr		
340	345	350
Ala Phe Ala Val Glu Gly Val Asn Thr Asp Ala Glu Phe Arg Glu Leu		
355	360	365
Val Lys Gly Trp Gly Leu Asn Asn Ala Thr Thr Asp Ile Leu Glu Ala		
370	375	380
Leu Tyr Pro Asp Ile Pro Gln Ile Gly Ile Pro Ala Ile Met Val Gly		
385	390	395
Arg Pro Pro Ser Gly Tyr Gly Asn Gln Tyr Lys Arg Val Ala Ala Phe		
405	410	415
Gln Gly Asp Val Asn Ile His Ala Ala Arg Arg Leu Thr Ser Gln Ile		
420	425	430
Trp Ser Ser Arg Asn Ile Ser Val Tyr Ser Tyr Met Phe Asp Val Ile		
435	440	445
Ser Pro Gly Tyr Gly Pro Ser Ala Gly Ser Tyr Ala Gly Ala Thr His		
450	455	460
Gly Thr Asp Ile Pro Tyr Val Phe Tyr Asn Leu Asp Gly Leu Gly Tyr		
465	470	475
Asp Ser Asn Asn Lys Ser Ile Glu Ser Ile Pro Asn Ser Tyr Ser Arg		
485	490	495
Met Ser Lys Ile Met Ser Arg Met Trp Val Ser Phe Val Thr Thr Leu		
500	505	510
Asp Pro Asn His Ser Gly Gly Met Val Pro His Pro Ile Pro Met Ile		
515	520	525
Ala Gln Cys Gln Thr Arg Ala Glu Ser Thr Ile Phe Leu Gly Thr Asn		
530	535	540
Val Gln Trp Pro Pro Tyr Asn Ile Asp Asn Pro Glu Ile Ile Phe Phe		
545	550	555
Asp Thr Asp Val Thr Asn Leu Thr Tyr Thr Trp Pro Ala Gly Leu Tyr		
565	570	575
Ala His Trp Trp		
580		

&lt;210&gt; 7

&lt;211&gt; 2769

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

## 21078W0.ST25.txt

&lt;400&gt; 7

gtgaacaatg	attagacttg	gagaacgtgg	tctccgattg	gaagtggact	atctattaa	60
tagtattgcc	aaggctttct	gatcgcaaaa	catattgtcc	tcccgtggtg	actggtttct	120
cgcctgatgt	gaatagtgtat	tatcaattta	tacccttcgt	cagcactgtat	tgaataagaa	180
cttacctcac	attgccctca	tttctatgtct	ggaaccatgc	acctatTTT	aagccatccg	240
gccgatctta	ctcacggtat	gggctgactt	tgtatcacaa	cccatacctg	tcgaccgtct	300
aaagtgggt	cagtgacaag	catgtgccc	gtcagcatca	tcagctcaac	aaattcttagc	360
caacaacgga	gatcagtggt	ccgacatttg	atgtagaatt	aaacccgcac	acgtcgaaat	420
ggcttcattc	tcggtcttag	tttccaatc	gaagctggtt	cagcggccag	acgcggagcg	480
tgggggtggg	accccgatt	ttccccacac	accttggctg	tgggtggcac	tttttcatta	540
gcctccatcc	tgtgcgcaga	tactagagaa	ctctacatca	tgccatcgag	gtttgttagt	600
tagattttt	aactagctga	gcgggtgtagg	tgcatgcccgt	acggtgagtt	tgtctatctt	660
ttgtatagcc	ggaagccgaa	ggtaccccg	gtcatggcta	tataaggctt	gtatatccca	720
tgctctggta	gatggacaa	caagaacggc	gatccgatag	aatcatggtg	cagggtgtgg	780
cttttggact	gctcgccctg	gctgcctctg	ctttggcac	ttatgcgccc	tactacgcga	840
atttgacatg	ggagcaacca	cgactctgt	ccaactggtc	caaccttacc	gtcgagacac	900
ggacagggac	gttcattggt	atgctcaatg	acacttaccc	agacgttcga	cagttctgc	960
gagttcccta	tgccaaggta	attctctcgc	tgtacacatg	tcatactgtg	tctgacatga	1020
ccagcctcct	attggggatt	taagatggct	tcctcctcat	cggttgaca	actcaagcag	1080
aacatatgac	tccaccttct	atggcccagg	taagtagtct	tccatacaac	tatgagcagt	1140
tccaattaac	ccgagttcag	cctgtccgca	gtatgttcca	gcagagagcg	atttttgaa	1200
tgaatatgaa	ccggagaatt	tgctgctcaa	tgtcggcgaa	aggctcaacc	agggctctac	1260
ggcatggtcc	tcgtcagagg	attgcctgtc	cctagcggt	tggactccat	cgtatgctaa	1320
tgagacatcc	aagctgccag	ttgcgtgtt	tgtcacggga	ggtgggtggca	tcacaggggg	1380
tatcaacatt	ccgtcccagc	tgccctctgc	ttgggtatct	cgctctcagg	agcatatcgt	1440
tgttaccatc	aattaccgcg	tcaatatttt	tggcagtaag	tatttgctct	atatttgcaa	1500
atatttagcct	gacatgtata	gatccaaat	cgcggtgcgtt	gaatgatacg	tcgcttacgc	1560
tgtatggacgt	gcfgcgtgct	gtggagtggg	tatatgagaa	cattgaagcg	ttcgggtggta	1620
atcccgaaaa	tattatggtc	agactacaag	tttcctctca	catgactaga	gctaacagta	1680
agcagctatg	gggacagtca	caagggtgtt	tgctgacgca	tctgtacacc	ctcgcatggc	1740
cagaagagcc	tcttgcgc	aagttccgc	tcatctccca	aggagcatct	gccacactca	1800
acctctctac	cacgcccgtat	gtgtaccaag	actttgacat	cgtggccaag	ggactaggct	1860
gcaattatgg	tgtatgtgcc	gaggccgagc	tggagtgcgt	gcgtgggatt	tcctgggtgc	1920
agatcgagga	gtatatcaac	cgctacaata	gctctccctc	tattgcttc	acgaactata	1980
ttcgtatgtt	cccatcttgc	tcttttaact	gccctacta	acaatatcag	ccgatgagaa	2040
atacatcttc	tccgacgaaa	gacagcgta	ccttgagcgg	aagggtgccc	gaggcccg	2100
aattcgatct	gacacggcgc	gagaattccc	tagcacaac	acgacactcg	taaatattga	2160
agaaggcgaa	tcagactgtc	tggcagtgc	tgaccttgc	ctacgtgcgt	ccattggct	2220
cgagacctat	cgctactact	gggctggat	gtccaatgac	tttccatact	gaagatagt	2280
ctaacataaa	caggcaactt	ctccaatatc	agtcccgta	cgtggctagg	agcattccac	2340
tggaccgacc	tgtatgtat	ttcggta	tataatctgg	acgtcgccga	gatctcgac	2400
ttggaagtgc	acacctctgc	cacgtgcaa	gattatctac	tcgccttct	gaaggactca	2460
tcaaccgtca	gcgagacggt	cgatggccg	ttatatctgg	gcaacgagac	caacggagga	2520
ctcatcctgg	agttcgtaa	cggcacagca	gtgcggacca	tcacaggtga	ctggctcgac	2580

## 21078W0.ST25.txt

gcgggatgtt tcaattcatc tatccattc agaatctggg ggttagcctat acacaccatc	2640
atcagagtat tatatacatc atatccacaa atccatctcc acctatatac ataaacccca	2700
actgaatcta caacagcgcc tggtccttct tcccctcccc ctcttaatt tccctcgccct	2760
tctccccat	2769

&lt;210&gt; 8

&lt;211&gt; 1623

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1623)

&lt;400&gt; 8

atg gtg cag ggt gtg gct ttt gga ctg ctc ggg ctg gct gcc tct gct	48
Met Val Gln Gly Val Ala Phe Gly Leu Leu Gly Leu Ala Ala Ser Ala	
1 5 10 15	

ttg ggc act tat gcg ccc tac tac gcg aat ttg aca tgg gag caa cca	96
Leu Gly Thr Tyr Ala Pro Tyr Tyr Ala Asn Leu Thr Trp Glu Gln Pro	
20 25 30	

cgg act ctg tcc aac tgg tcc aac ctt acc gtc gag aca cgg aca ggg	144
Arg Thr Leu Ser Asn Trp Ser Asn Leu Thr Val Glu Thr Arg Thr Gly	
35 40 45	

acg ttc att ggt atg ctc aat gac act tac cca gac gtt cga cag ttt	192
Thr Phe Ile Gly Met Leu Asn Asp Thr Tyr Pro Asp Val Arg Gln Phe	
50 55 60	

ctg cga gtt cct tat gcc aag cct cct att ggg gat tta aga tgg ctt	240
Leu Arg Val Pro Tyr Ala Lys Pro Pro Ile Gly Asp Leu Arg Trp Leu	
65 70 75 80	

cct cct cat cgg ctt gac aac tca agc aga aca tat gac tcc acc ttc	288
Pro Pro His Arg Leu Asp Asn Ser Ser Arg Thr Tyr Asp Ser Thr Phe	
85 90 95	

tat ggc cca gcc tgt ccg cag tat gtt cca gca gag agc gat ttt tgg	336
Tyr Gly Pro Ala Cys Pro Gln Tyr Val Pro Ala Glu Ser Asp Phe Trp	
100 105 110	

aat gaa tat gaa ccg gag aat ttg ctg ctc aat gtc ggc gaa agg ctc	384
Asn Glu Tyr Glu Pro Glu Asn Leu Leu Asn Val Gly Glu Arg Leu	
115 120 125	

aac cag ggc tct acg gca tgg tcc tcg tca gag gat tgc ctg tcc cta	432
Asn Gln Gly Ser Thr Ala Trp Ser Ser Ser Glu Asp Cys Leu Ser Leu	
130 135 140	

gcg gta tgg act cca tcg tat gct aat gag aca tcc aag ctg cca gtt	480
---	-----

## 21078WO.ST25.txt

Ala Val Trp Thr Pro Ser Tyr Ala Asn Glu Thr Ser Lys Leu Pro Val				
145	150	155	160	
gct ctg ttt gtc acg gga ggt ggt ggc atc aca ggg ggt atc aac att				528
Ala Leu Phe Val Thr Gly Gly Gly Ile Thr Gly Gly Ile Asn Ile				
165	170	175		
ccg tcc cag ctg ccc tct gct tgg gta tct cgc tct cag gag cat atc				576
Pro Ser Gln Leu Pro Ser Ala Trp Val Ser Arg Ser Gln Glu His Ile				
180	185	190		
gtt gtt acc atc aat tac cgc gtc aat att ttt ggc aat ccc aaa tcg				624
Val Val Thr Ile Asn Tyr Arg Val Asn Ile Phe Gly Asn Pro Lys Ser				
195	200	205		
cgt gcg ttg aat gat acg tcg ctt acg ctg atg gac gtg cgc gct gct				672
Arg Ala Leu Asn Asp Thr Ser Leu Thr Leu Met Asp Val Arg Ala Ala				
210	215	220		
gtg gag tgg gta tat gag aac att gaa gcg ttc ggt ggt aat ccc gaa				720
Val Glu Trp Val Tyr Glu Asn Ile Glu Ala Phe Gly Gly Asn Pro Glu				
225	230	235	240	
aat att atg gtc aga cta caa gtt tcc tct cac atg act aga gct aac				768
Asn Ile Met Val Arg Leu Gln Val Ser Ser His Met Thr Arg Ala Asn				
245	250	255		
agt aag cag cta tgg gga cag tca caa ggt gct ttg ctg acg cat ctg				816
Ser Lys Gln Leu Trp Gly Gln Ser Gln Gly Ala Leu Leu Thr His Leu				
260	265	270		
tac acc ctc gca tgg cca gaa gag cct ctt gcc gcc aag ttc ggc gtc				864
Tyr Thr Leu Ala Trp Pro Glu Glu Pro Leu Ala Ala Lys Phe Gly Val				
275	280	285		
atc tcc caa gga gca tct gcc aca ctc aac ctc tct acc acg ccc gat				912
Ile Ser Gln Gly Ala Ser Ala Thr Leu Asn Leu Ser Thr Thr Pro Asp				
290	295	300		
gtg tac caa gac ttt gac atc gtg gcc aag gga cta ggc tgc aat tat				960
Val Tyr Gln Asp Phe Asp Ile Val Ala Lys Gly Leu Gly Cys Asn Tyr				
305	310	315	320	
ggt gat gat gcc gag gcc gag ctg gag tgc atg cgt ggg att tcc tgg				1008
Gly Asp Asp Ala Glu Ala Glu Leu Glu Cys Met Arg Gly Ile Ser Trp				
325	330	335		
gtg cag atc gag gag tat atc aac cgc tac aat agc tct cct tct att				1056
Val Gln Ile Glu Glu Tyr Ile Asn Arg Tyr Asn Ser Ser Pro Ser Ile				
340	345	350		
gct ttc acg aac tat att ccc gat gag aaa tac atc ttc tcc gac gaa				1104
Ala Phe Thr Asn Tyr Ile Pro Asp Glu Lys Tyr Ile Phe Ser Asp Glu				
355	360	365		
aga cag cgt tac ctt gag cggt aag gtt gcc cga ggc ccg tca att cga				1152
Arg Gln Arg Tyr Leu Glu Arg Lys Val Ala Arg Gly Pro Ser Ile Arg				
370	375	380		

## 21078WO.ST25.txt

tct gac acg gcg cga gaa ttc cct	agc aca aac acg acc tca gta aat	1200
Ser Asp Thr Ala Arg Glu Phe Pro Ser Thr Asn Thr Thr Ser Val Asn		
385 390 395 400		
att gaa gaa ggc gaa tca gac tgt ctg gca gtg act gac ctt gcg cta		1248
Ile Glu Glu Gly Glu Ser Asp Cys Leu Ala Val Thr Asp Leu Ala Leu		
405 410 415		
cgt gcg tcc att ggg ctc gag acc tat cgc tac tac tgg gct ggc aac		1296
Arg Ala Ser Ile Gly Leu Glu Thr Tyr Arg Tyr Tyr Trp Ala Gly Asn		
420 425 430		
ttc tcc aat atc agt ccc gta ccg tgg cta gga gca ttc cac tgg acc		1344
Phe Ser Asn Ile Ser Pro Val Pro Trp Leu Gly Ala Phe His Trp Thr		
435 440 445		
gac ctg ctg atg atc ttc ggt acg tat aat ctg gac gtc ggc gag atc		1392
Asp Leu Leu Met Ile Phe Gly Thr Tyr Asn Leu Asp Val Gly Glu Ile		
450 455 460		
tcg cag ttg gaa gtc gac acc tct gcc acg atg caa gat tat cta ctc		1440
Ser Gln Leu Glu Val Asp Thr Ser Ala Thr Met Gln Asp Tyr Leu Leu		
465 470 475 480		
gcc ttt ctg aag gac tca tca acc gtc agc gag acg gtc gga tgg ccg		1488
Ala Phe Leu Lys Asp Ser Ser Thr Val Ser Glu Thr Val Gly Trp Pro		
485 490 495		
tta tat ctg ggc aac gag acc aac gga gga ctc atc ctg gag ttc ggt		1536
Leu Tyr Leu Gly Asn Glu Thr Asn Gly Gly Leu Ile Leu Glu Phe Gly		
500 505 510		
aac ggc aca gca gtg cg acc atc aca ggt gac tgg ctc gac gcg gga		1584
Asn Gly Thr Ala Val Arg Thr Ile Thr Gly Asp Trp Leu Asp Ala Gly		
515 520 525		
tgt ttc aat tca tct atc cca ttc aga atc tgg ggg tag		1623
Cys Phe Asn Ser Ser Ile Pro Phe Arg Ile Trp Gly		
530 535 540		

&lt;210&gt; 9

&lt;211&gt; 540

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 9

Met Val Gln Gly Val Ala Phe Gly Leu Leu Gly Leu Ala Ala Ser Ala

1 5 10 15

Leu Gly Thr Tyr Ala Pro Tyr Tyr Ala Asn Leu Thr Trp Glu Gln Pro

20 25 30

Arg Thr Leu Ser Asn Trp Ser Asn Leu Thr Val Glu Thr Arg Thr Gly

35 40 45

## 21078WO.ST25.txt

Thr Phe Ile Gly Met Leu Asn Asp Thr Tyr Pro Asp Val Arg Gln Phe  
 50 55 60  
 Leu Arg Val Pro Tyr Ala Lys Pro Pro Ile Gly Asp Leu Arg Trp Leu  
 65 70 75 80  
 Pro Pro His Arg Leu Asp Asn Ser Ser Arg Thr Tyr Asp Ser Thr Phe  
 85 90 95  
 Tyr Gly Pro Ala Cys Pro Gln Tyr Val Pro Ala Glu Ser Asp Phe Trp  
 100 105 110  
 Asn Glu Tyr Glu Pro Glu Asn Leu Leu Leu Asn Val Gly Glu Arg Leu  
 115 120 125  
 Asn Gln Gly Ser Thr Ala Trp Ser Ser Ser Glu Asp Cys Leu Ser Leu  
 130 135 140  
 Ala Val Trp Thr Pro Ser Tyr Ala Asn Glu Thr Ser Lys Leu Pro Val  
 145 150 155 160  
 Ala Leu Phe Val Thr Gly Gly Gly Ile Thr Gly Gly Ile Asn Ile  
 165 170 175  
 Pro Ser Gln Leu Pro Ser Ala Trp Val Ser Arg Ser Gln Glu His Ile  
 180 185 190  
 Val Val Thr Ile Asn Tyr Arg Val Asn Ile Phe Gly Asn Pro Lys Ser  
 195 200 205  
 Arg Ala Leu Asn Asp Thr Ser Leu Thr Leu Met Asp Val Arg Ala Ala  
 210 215 220  
 Val Glu Trp Val Tyr Glu Asn Ile Glu Ala Phe Gly Gly Asn Pro Glu  
 225 230 235 240  
 Asn Ile Met Val Arg Leu Gln Val Ser Ser His Met Thr Arg Ala Asn  
 245 250 255  
 Ser Lys Gln Leu Trp Gly Gln Ser Gln Gly Ala Leu Leu Thr His Leu  
 260 265 270  
 Tyr Thr Leu Ala Trp Pro Glu Glu Pro Leu Ala Ala Lys Phe Gly Val  
 275 280 285  
 Ile Ser Gln Gly Ala Ser Ala Thr Leu Asn Leu Ser Thr Thr Pro Asp  
 290 295 300  
 Val Tyr Gln Asp Phe Asp Ile Val Ala Lys Gly Leu Gly Cys Asn Tyr  
 305 310 315 320  
 Gly Asp Asp Ala Glu Ala Glu Leu Glu Cys Met Arg Gly Ile Ser Trp  
 325 330 335  
 Val Gln Ile Glu Glu Tyr Ile Asn Arg Tyr Asn Ser Ser Pro Ser Ile  
 340 345 350  
 Ala Phe Thr Asn Tyr Ile Pro Asp Glu Lys Tyr Ile Phe Ser Asp Glu  
 355 360 365  
 Arg Gln Arg Tyr Leu Glu Arg Lys Val Ala Arg Gly Pro Ser Ile Arg  
 370 375 380  
 Ser Asp Thr Ala Arg Glu Phe Pro Ser Thr Asn Thr Thr Ser Val Asn  
 385 390 395 400

21078WO.ST25.txt

<210> 10  
<211> 3235  
<212> DNA  
<213> *Aspergillus niger*

<400> 10	
gttttcaatt tggactgaat tttggcgca tttcttgtat aaaattaaaa ggggcgttga	60
ctggattttg gtacttggga ttatttctta gctttgactg tacatagttt gggcgtggtt	120
tgatagccga cgatcgcccg acccacgaac cagatttgc tatgattaca ttccttcaat	180
tttggtccga gtcccaaccc gccttcaac cccaacaact acaagcacgt tgtgttgct	240
acattgactc actcgatatt gctgaaccat gcaggccgcc caactgagtt attacaccaa	300
gcatgcgaat cgaaaagttc gacaaagcgg gtgaaatgtc cgagttggcg aaccaaagcg	360
caacggtcga ggctccttc cccgcagagg cagccattct gcagccttgc aactgcgggg	420
gaaacggcat ttgatcaact cggcactgat gcagtgacca acaggatgtt agcaatgttgc	480
gcctaataata ttcttactga tctgctgata cgtccctccc ttgcatcagc ctcgggttgc	540
gcatgagaac gggttcgaac gttcctggc caccgggttgc gctgtatatt ctccgccccac	600
gctgtctgtc cccctgtatgg gaaaccttcg gatcagcgat catcaggccca gttggctatg	660
agaataagggg ctttgctgtc ttgatgccta aaatgcaggt ctcatagcaa gatccacagc	720
cgaggaggca catggcgatg tcgaaaccca tgggagctga ttttcgggtt ctcggatcgat	780
gctccaagac atagaaggat attgagact tgaaacgaag gggtaaaaaa tggaactgtat	840
tatagagttt ctcccagccc gatcccgagag cctatgaccc atagcggtac agatcatggc	900
catcatgaag gccctcctt ggctctccct ttccctcgcc gtctggcga ctccagttca	960
acgggatgca gctcctactg tcactattgc gcatccatcg gccaccgtca ttggaaaatc	1020
tggcaatgtc gagagcttca acaatattcc ctttgcgcag gcccccacag gctcgctgcg	1080

## 21078WO.ST25.txt

tctgaagccc	ccacaaccct	tggaaactgc	cctcggca	gttcaggcca	caggagcctc	1140
gcaatcggt	cccgagatgt	acttcaccac	ggatgagagc	gaattcccg	catcggtcat	1200
tggcctc	cttgcgttcc	ctttggtaca	gtcggctacc	aatgtctcg	aggattgcct	1260
gaacattgac	attcggcg	cggccggac	caccgcggac	tcgaagctgc	ctgtgctggt	1320
ctggatctt	ggcggaggct	ttgaacttgg	ttcaaaggcg	atgtatgatg	gtacaacgat	1380
gttatcatcg	tcgatagaca	agaacatgcc	tatcggttt	gtagcaatga	attatcgct	1440
gggaggtttc	gggttctgc	ccggaaagga	gatcctggag	gacgggtccg	cgaacctagg	1500
gctcctggac	caacgcctt	ccctgcagt	gttgccgac	aacatcgagg	ccttggtgg	1560
agacccggac	aaggtgacga	tttgggaga	atcagcagga	gccattccg	tttttgcata	1620
gatgatctt	tacgacggaa	acatca	caaggataag	cccttgttcc	ggggggccat	1680
catggactcc	ggtgtgtt	ttccgcaga	ccccgtcgat	ggggtaagg	gacagcaagt	1740
atatgatgcg	gtatgttgc	ttcctttt	aacgacaccc	tagttgtct		1800
gcgtgaacta	gactacaccg	acttcctcaa	tgcggcaa	tccgtgcag	gcattttaa	1860
ctaccattct	gtggcg	ttatgtgc	tcgaccggac	gggacggcg	tgtcgccatc	1920
accggacgtt	ttggcaaa	caggaaata	tgctcggtc	ccgttcatcg	ttggcgacca	1980
agaggatgag	gggacattat	tcgcctgtt	tcagtccaa	attacgacga	tcgacgaggt	2040
ggtcgactac	ctggcctcat	acttcttcta	tgacgctagc	cgagagcagc	ttgaagaact	2100
agtggccctg	tacccagaca	ccaccacgt	cgggtctccg	ttcaggacag	gcgcggccaa	2160
caactggtat	ccgcaattt	agcgattggc	ccgcattctc	ggcgacttgg	tcttaccat	2220
tacccggcgg	gcattcct	cgtatgcaga	ggaaatctcc	cctgatctc	cgaactggc	2280
gtacctggcg	acctatgact	atggcacccc	agttctgggg	accttccacg	gaagtgcac	2340
gctcaggtg	ttctatggg	tcaagccaaa	ctatgcag	agttcttagcc	acacgtacta	2400
tctgagctt	gtgtatacgc	tggatccgaa	ctccaaccgg	ggggagtaca	ttgagtggcc	2460
gcagtggaa	gaatcgccg	agttgatgaa	tttcggagcg	aacgacgcca	gtctccttac	2520
ggatgatttc	cgaacggg	catatgagtt	catcctgcag	aataccgcgg	cgttccacat	2580
ctgatgccat	tggcggaggg	gtccggacgg	tcaggaactt	agccttatga	gatgaatgat	2640
ggacgtgtct	ggcctcgaa	aaggatata	ggggatcatg	atagtactag	ccatattaat	2700
gaagggcata	taccacgcgt	tggacctgcg	ttatagcttc	ccgttagtta	tagtaccatc	2760
gttataccag	ccaatcaagt	caccacgcac	gaccggggac	ggcgaatccc	cggaaattga	2820
aagaaattgc	atcccaggcc	agtgaggcca	gcgattggcc	acctctccaa	ggcacaggc	2880
cattctgcag	cgtgggtgg	ttcatcgca	tttccccccg	cccgccccg	caccgcata	2940
ggctggttct	cccacaccat	cggagattcg	tcgccta	tctcgccgt	tcacaagctg	3000
aagagcttga	agtggcgaga	tgtctctgca	ggaattcaag	ctagatgct	agcgatattg	3060
catggcaata	tgtgttgatg	catgtgttcc	ttccttcagc	ttcccctcg	gcagatgagg	3120
tttggctata	aattgaagt	gttggtcggg	gttccgtgag	gggctgaagt	gcttcctccc	3180
ttttagacgc	aactgagagc	ctgagcttca	tccca	cattacac	cagca	3235

&lt;210&gt; 11

&lt;211&gt; 1689

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

## 21078WO.ST25.txt

&lt;221&gt; CDS

&lt;222&gt; (1)..(1689)

&lt;400&gt; 11

atg	gcc	atc	atg	aag	gcc	ctc	ctt	tgg	ctc	tcc	ctt	tcc	ctc	gcc	gtc		48
Met	Ala	Ile	Met	Lys	Ala	Leu	Leu	Trp	Leu	Ser	Leu	Ser	Leu	Ala	Val		
1			5				10								15		
tgg	gcg	act	cca	gtt	caa	cgg	gat	gca	gct	cct	act	gtc	act	att	gcg		96
Trp	Ala	Thr	Pro	Val	Gln	Arg	Asp	Ala	Ala	Pro	Thr	Val	Thr	Ile	Ala		
			20				25								30		
cat	cca	tcg	gcc	acc	gtc	att	gga	aaa	tct	ggc	aat	gtc	gag	agc	ttc		144
His	Pro	Ser	Ala	Thr	Val	Ile	Gly	Lys	Ser	Gly	Asn	Val	Glu	Ser	Phe		
			35				40								45		
aac	aat	att	ccc	ttt	gcf	cag	gcc	ccc	aca	ggc	tcg	ctg	cgt	ctg	aag		192
Asn	Asn	Ile	Pro	Phe	Ala	Gln	Ala	Pro	Thr	Gly	Ser	Leu	Arg	Leu	Lys		
			50				55								60		
ccc	cca	caa	ccc	ttg	gaa	act	gcc	ctc	ggc	act	gtt	cag	gcc	aca	gga		240
Pro	Pro	Gln	Pro	Leu	Glu	Thr	Ala	Leu	Gly	Thr	Val	Gln	Ala	Thr	Gly		
			65				70								80		
gcc	tcg	caa	tcg	tgt	ccg	cag	atg	tac	ttc	acc	acg	gat	gag	agc	gaa		288
Ala	Ser	Gln	Ser	Cys	Pro	Gln	Met	Tyr	Phe	Thr	Thr	Asp	Glu	Ser	Glu		
							85								95		
ttc	ccg	aca	tcg	gtc	att	ggc	ctc	ctc	gct	gat	ctc	cct	ttg	gta	cag		336
Phe	Pro	Thr	Ser	Val	Ile	Gly	Leu	Leu	Ala	Asp	Leu	Pro	Leu	Val	Gln		
					100		105								110		
tcg	gct	acc	aat	gct	ctc	gag	gat	tgc	ctg	aac	att	gac	att	cg	cgt		384
Ser	Ala	Thr	Asn	Ala	Leu	Glu	Asp	Cys	Leu	Asn	Ile	Asp	Ile	Arg	Arg		
					115		120								125		
ccg	gcc	ggg	acc	acc	gcf	gac	tcg	aag	ctg	cct	gtg	ctg	gtc	tgg	atc		432
Pro	Ala	Gly	Thr	Thr	Ala	Asp	Ser	Lys	Leu	Pro	Val	Leu	Val	Trp	Ile		
					130		135								140		
ttt	ggc	gga	ggc	ttt	gaa	ctt	ggt	tca	aag	gcf	atg	tat	gat	ggt	aca		480
Phe	Gly	Gly	Gly	Phe	Glu	Leu	Gly	Ser	Lys	Ala	Met	Tyr	Asp	Gly	Thr		
					145		150								160		
acg	atg	gta	tca	tcg	tcg	ata	gac	aag	aac	atg	cct	atc	gtg	ttt	gta		528
Thr	Met	Val	Ser	Ser	Ile	Asp	Lys	Asn	Met	Pro	Ile	Val	Phe	Val			
					165		170								175		
gca	atg	aat	tat	cgc	gtg	gga	ggt	ttc	ggg	ttc	ttg	ccc	gga	aag	gag		576
Ala	Met	Asn	Tyr	Arg	Val	Gly	Gly	Phe	Gly	Phe	Leu	Pro	Gly	Lys	Glu		
					180		185								190		
atc	ctg	gag	gac	ggg	tcc	gcf	aac	cta	ggg	ctc	ctg	gac	caa	cgc	ctt		624
Ile	Leu	Glu	Asp	Gly	Ser	Ala	Asn	Leu	Gly	Leu	Leu	Asp	Gln	Arg	Leu		
					195		200								205		
gcc	ctg	cag	tgg	gtt	gcc	gac	aac	atc	gag	gcc	ttt	ggt	gga	gac	ccg		672

## 21078WO.ST25.txt

Ala Leu Gln Trp Val Ala Asp Asn Ile Glu Ala Phe Gly Gly Asp Pro			
210	215	220	
gac aag gtg acg att tgg gga gaa tca gca gga gcc att tcc gtt ttt			720
Asp Lys Val Thr Ile Trp Gly Glu Ser Ala Gly Ala Ile Ser Val Phe			
225	230	235	240
gat cag atg atc ttg tac gac gga aac atc act tac aag gat aag ccc			768
Asp Gln Met Ile Leu Tyr Asp Gly Asn Ile Thr Tyr Lys Asp Lys Pro			
245	250	255	
ttg ttc cgg ggg gcc atc atg gac tcc ggt agt gtt gtt ccc gca gac			816
Leu Phe Arg Gly Ala Ile Met Asp Ser Gly Ser Val Val Pro Ala Asp			
260	265	270	
ccc gtc gat ggg gtc aag gga cag caa gta tat gat gcg gta gtg gaa			864
Pro Val Asp Gly Val Lys Gly Gln Gln Val Tyr Asp Ala Val Val Glu			
275	280	285	
tct gca ggc tgt tcc tct tct aac gac acc cta gct tgt ctg cgt gaa			912
Ser Ala Gly Cys Ser Ser Asn Asp Thr Leu Ala Cys Leu Arg Glu			
290	295	300	
cta gac tac acc gac ttc ctc aat gcg gca aac tcc gtg cca ggc att			960
Leu Asp Tyr Thr Asp Phe Leu Asn Ala Ala Asn Ser Val Pro Gly Ile			
305	310	315	320
tta agc tac cat tct gtg gcg tta tca tat gtg cct cga ccg gac ggg			1008
Leu Ser Tyr His Ser Val Ala Leu Ser Tyr Val Pro Arg Pro Asp Gly			
325	330	335	
acg gcg ttg tcg gca tca ccg gac gtt ttg ggc aaa gca ggg aaa tat			1056
Thr Ala Leu Ser Ala Ser Pro Asp Val Leu Gly Lys Ala Gly Lys Tyr			
340	345	350	
gct cgg gtc ccg ttc atc gtg ggc gac caa gag gat gag ggg acc tta			1104
Ala Arg Val Pro Phe Ile Val Gly Asp Gln Glu Asp Glu Gly Thr Leu			
355	360	365	
ttc gcc ttg ttt cag tcc aac att acg acg atc gac gag gtg gtc gac			1152
Phe Ala Leu Phe Gln Ser Asn Ile Thr Thr Ile Asp Glu Val Val Asp			
370	375	380	
tac ctg gcc tca tac ttc ttc tat gac gct agc cga gag cag ctt gaa			1200
Tyr Leu Ala Ser Tyr Phe Phe Tyr Asp Ala Ser Arg Glu Gln Leu Glu			
385	390	395	400
gaa cta gtg gcc ctg tac cca gac acc acc acg tac ggg tct ccg ttc			1248
Glu Leu Val Ala Leu Tyr Pro Asp Thr Thr Tyr Ser Pro Phe			
405	410	415	
agg aca ggc gcg gcc aac aac tgg tat ccg caa ttt aag cga ttg gcc			1296
Arg Thr Gly Ala Ala Asn Asn Trp Tyr Pro Gln Phe Lys Arg Leu Ala			
420	425	430	
gcc att ctc ggc gac ttg gtc ttc acc att acc ccg ccg gca ttc ctc			1344
Ala Ile Leu Gly Asp Leu Val Phe Thr Ile Thr Arg Arg Ala Phe Leu			
435	440	445	

## 21078WO.ST25.txt

tcg tat gca gag gaa atc tcc cct gat ctt ccg aac tgg tcg tac ctg		1392
Ser Tyr Ala Glu Glu Ile Ser Pro Asp Leu Pro Asn Trp Ser Tyr Leu		
450	455	460
gcg acc tat gac tat ggc acc cca gtt ctg ggg acc ttc cac gga agt		1440
Ala Thr Tyr Asp Tyr Gly Thr Pro Val Leu Gly Thr Phe His Gly Ser		
465	470	475
gac ctg ctg cag gtg ttc tat ggg atc aag cca aac tat gca gct agt		1488
Asp Leu Leu Gln Val Phe Tyr Gly Ile Lys Pro Asn Tyr Ala Ala Ser		
485	490	495
tct agc cac acg tac tat ctg agc ttt gtg tat acg ctg gat ccg aac		1536
Ser Ser His Thr Tyr Tyr Leu Ser Phe Val Tyr Thr Leu Asp Pro Asn		
500	505	510
tcc aac cg <sup>g</sup> ggg gag tac att gag tgg ccg cag tgg aag gaa tcg cg <sup>g</sup>		1584
Ser Asn Arg Gly Glu Tyr Ile Glu Trp Pro Gln Trp Lys Glu Ser Arg		
515	520	525
cag ttg atg aat ttc gga gc <sup>g</sup> aac gac gcc agt ctc ctt acg gat gat		1632
Gln Leu Met Asn Phe Gly Ala Asn Asp Ala Ser Leu Leu Thr Asp Asp		
530	535	540
ttc cgc aac ggg aca tat gag ttc atc ctg cag aat acc gc <sup>g</sup> gc <sup>g</sup> ttc		1680
Phe Arg Asn Gly Thr Tyr Glu Phe Ile Leu Gln Asn Thr Ala Ala Phe		
545	550	555
cac atc tga		1689
His Ile		

&lt;210&gt; 12

&lt;211&gt; 562

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 12

Met Ala Ile Met Lys Ala Leu Leu Trp Leu Ser Leu Ser Leu Ala Val			
1	5	10	15
Trp Ala Thr Pro Val Gln Arg Asp Ala Ala Pro Thr Val Thr Ile Ala			
20	25	30	
His Pro Ser Ala Thr Val Ile Gly Lys Ser Gly Asn Val Glu Ser Phe			
35	40	45	
Asn Asn Ile Pro Phe Ala Gln Ala Pro Thr Gly Ser Leu Arg Leu Lys			
50	55	60	
Pro Pro Gln Pro Leu Glu Thr Ala Leu Gly Thr Val Gln Ala Thr Gly			
65	70	75	80
Ala Ser Gln Ser Cys Pro Gln Met Tyr Phe Thr Thr Asp Glu Ser Glu			
85	90	95	
Phe Pro Thr Ser Val Ile Gly Leu Leu Ala Asp Leu Pro Leu Val Gln			

## 21078W0.ST25.txt

100	105	110
Ser Ala Thr Asn Ala Leu Glu Asp Cys Leu Asn Ile Asp Ile Arg Arg		
115	120	125
Pro Ala Gly Thr Thr Ala Asp Ser Lys Leu Pro Val Leu Val Trp Ile		
130	135	140
Phe Gly Gly Gly Phe Glu Leu Gly Ser Lys Ala Met Tyr Asp Gly Thr		
145	150	155
160		
Thr Met Val Ser Ser Ser Ile Asp Lys Asn Met Pro Ile Val Phe Val		
165	170	175
Ala Met Asn Tyr Arg Val Gly Gly Phe Glu Leu Pro Gly Lys Glu		
180	185	190
Ile Leu Glu Asp Gly Ser Ala Asn Leu Gly Leu Leu Asp Gln Arg Leu		
195	200	205
Ala Leu Gln Trp Val Ala Asp Asn Ile Glu Ala Phe Gly Gly Asp Pro		
210	215	220
Asp Lys Val Thr Ile Trp Gly Glu Ser Ala Gly Ala Ile Ser Val Phe		
225	230	235
240		
Asp Gln Met Ile Leu Tyr Asp Gly Asn Ile Thr Tyr Lys Asp Lys Pro		
245	250	255
Leu Phe Arg Gly Ala Ile Met Asp Ser Gly Ser Val Val Pro Ala Asp		
260	265	270
Pro Val Asp Gly Val Lys Gly Gln Gln Val Tyr Asp Ala Val Val Glu		
275	280	285
Ser Ala Gly Cys Ser Ser Ser Asn Asp Thr Leu Ala Cys Leu Arg Glu		
290	295	300
Leu Asp Tyr Thr Asp Phe Leu Asn Ala Ala Asn Ser Val Pro Gly Ile		
305	310	315
320		
Leu Ser Tyr His Ser Val Ala Leu Ser Tyr Val Pro Arg Pro Asp Gly		
325	330	335
Thr Ala Leu Ser Ala Ser Pro Asp Val Leu Gly Lys Ala Gly Lys Tyr		
340	345	350
Ala Arg Val Pro Phe Ile Val Gly Asp Gln Glu Asp Glu Gly Thr Leu		
355	360	365
Phe Ala Leu Phe Gln Ser Asn Ile Thr Thr Ile Asp Glu Val Val Asp		
370	375	380
Tyr Leu Ala Ser Tyr Phe Phe Tyr Asp Ala Ser Arg Glu Gln Leu Glu		
385	390	395
400		
Glu Leu Val Ala Leu Tyr Pro Asp Thr Thr Thr Tyr Gly Ser Pro Phe		
405	410	415
Arg Thr Gly Ala Ala Asn Asn Trp Tyr Pro Gln Phe Lys Arg Leu Ala		
420	425	430
Ala Ile Leu Gly Asp Leu Val Phe Thr Ile Thr Arg Arg Ala Phe Leu		
435	440	445
Ser Tyr Ala Glu Glu Ile Ser Pro Asp Leu Pro Asn Trp Ser Tyr Leu		

## 21078WO.ST25.txt

450	455	460
Ala	Thr Tyr Asp Tyr Gly Thr Pro Val Leu Gly Thr Phe His Gly Ser	
465	470	475
Asp	Leu Leu Gln Val Phe Tyr Gly Ile Lys Pro Asn Tyr Ala Ala Ser	480
	485	490
Ser	Ser His Thr Tyr Tyr Leu Ser Phe Val Tyr Thr Leu Asp Pro Asn	
	500	505
Ser	Ser Asn Arg Gly Glu Tyr Ile Glu Trp Pro Gln Trp Lys Glu Ser Arg	
	515	520
Gln	Gln Leu Met Asn Phe Gly Ala Asn Asp Ala Ser Leu Leu Thr Asp Asp	
	530	535
Phe	Phe Arg Asn Gly Thr Tyr Glu Phe Ile Leu Gln Asn Thr Ala Ala Phe	
	545	550
His	His Ile	560

&lt;210&gt; 13

&lt;211&gt; 2097

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;400&gt; 13

cctggctgac	gctataccga	agacgatgtc	gatgtcgct	ttgctcagag	cccccgagtc	60
gtttggggca	cgtcaagaaa	gtagtcttcg	ctgctgctt	aagacatgtat	caggacacgc	120
ggttcgacct	tcgagtgtac	atgatatccg	tagaatttgc	ttgtgactac	caaggcatat	180
gttagttcgt	gcagtggtaa	aagcggttcc	tcttcttcaa	tctgcgaggt	ggagatgcct	240
actatgatcg	tcatccaact	tggtgtctac	aagacgaaca	caagcttagt	tccgacgaac	300
cagtgaaaac	tctgtaagat	atataagagc	atcaagagtc	ggacttgctt	aggagagtgg	360
atagttgtt	atgctcgccg	aagctctcat	atagtataga	tatgaagtat	cggtgagtcg	420
tagtagtc	tgtatttat	agggagaggc	tgaatgggt	gggtcatgt	aatttccaca	480
taatagcgat	taaagcccta	gatcgagggt	atcttgaggc	ataaatgata	gtatcagtgg	540
acatatcctg	agatgaggat	gatatgagat	gatagagatg	aggaagaaag	aggaaaagaga	600
gaggcaagaa	cagagatttt	tataccttgc	cagagcagcc	catccgtcac	tgaattcagg	660
catcttcact	ccatactatc	acgagtcaac	gtgaagttgt	ataagcttag	tgacaggccg	720
cagtgacgat	gatccgtcac	tgccgtggct	atccgcact	gatcttgcta	tccgtgactg	780
cgttgactct	ggtgaaccaa	gtgttggga	aggggtgaaa	atgaagctga	agcgggtcag	840
ggaacattcc	aagcaacact	agacgagtca	gcgacgagtc	agcgatccac	tcggtctcac	900
acgctcccaa	tagtctcaat	ttgggtccaa	tggcaactaa	gtattccatc	cacttttaat	960
taaagtgtatc	agcggtgac	gaattcacat	gctggatctg	gtacagatca	gattaatatc	1020
tcctggata	cgtgaaggc	ccacccagg	attcacgata	aatttctgg	gactgccagc	1080
tcgaatggca	ttctccgtca	ctctacacct	gccgttgg	aatttctccg	acctctaatt	1140
gtcaatttct	gccaatgc	gtctatcatc	gctggccctg	gatccagcg	ccatcctacc	1200
cgccttaggc	tacagcatca	acgacttctc	ctgcaatagc	accgaacacc	cgaatccagt	1260
tgtgctctta	catgggctag	gcccaccta	ctacgaagac	ttgaattacc	tgcaagttg	1320

21078WO.ST25.txt

gctacagacc	caaggctatt	gcacttacgc	caaaacctac	ggtgcatatg	aaggcttccc	1380
cttgcggc	ggcctaagg	ccatcgccga	atcgccacg	gaaatcgccg	cgtacatccg	1440
cgaggtaaaa	gaaaagacgg	gcccgcacaa	gattgacctt	gtcggtcact	ccgaaggcgc	1500
cttccagacc	ctctacgtcc	ctaagttcga	ggatggtatac	tcggagatgc	tggataagct	1560
ggtggccatt	gcacctccca	ccagaggcac	caacttggcg	ggatatctatg	acatcgata	1620
tgttctggta	aatctatcgc	gcatctgtat	aggcgacgtc	ctggataccg	tgggctgcgc	1680
cgcctgtat	gatctgggtc	cgatggagc	agcgattgac	cgcttgaacg	atggcgagcc	1740
tatcgtgcag	ccggaaata	atctaacggt	gattgcatcg	cggtccgacg	aattggtcac	1800
cccaaccacc	acctccttcg	tgcataaga	tgggtgacc	aatgaatggg	tgcaagacac	1860
ttgtcctcta	gaccctgtcg	gtcatatcg	tgaggcatac	gatctgaacg	tctggaaattt	1920
ggtaaaaaac	gccttgact	ctacgcccga	gcgtgaggtc	gtctgctcgc	tggatctcc	1980
cggcagggtga	gactatcatc	ttctgaaaat	ttgttatataa	gcatttatat	ttggataccc	2040
ggttaccagt	cattagtqtc	ataatgtata	ataatatcac	cacaacttcc	tccaagc	2097

<210> 14

<211> 834

<212> DNA

<213> Aspergillus niger

<220>

<221> CDS

<222> (1) .. (834)

<400> 14

atg cgt cta tca tcg ctg gcc gca tcc agc gcc atc cta ccc gcc  
Met Arg Leu Ser Ser Leu Ala Leu Ala Ser Ser Ala Ile Leu Pro Ala  
1 5 10 15

tta ggc tac agc atc aac gac ttc tcc tgc aat agc acc gaa cac ccg	96
Leu Gly Tyr Ser Ile Asn Asp Phe Ser Cys Asn Ser Thr Glu His Pro	
20                    25                    30	

aat cca gtt gtg ctc cta cat ggg cta ggc gcc acc tac tac gaa gac 144  
Asn Pro Val Val Leu Leu His Gly Leu Gly Ala Thr Tyr Tyr Glu Asp  
35 40 45

ttg aat tac ctg caa ggt tgg cta cag acc caa ggc tat tgc act tac 192  
Leu Asn Tyr Leu Gln Gly Trp Leu Gln Thr Gln Gly Tyr Cys Thr Tyr  
50 55 60

65            .            70            .            75            80  
 gcc aaa acc tac ggt gca tat gaa ggc ttc ccc ttt gtc ggc ggc ctc      240  
 Ala Lys Thr Tyr Gly Ala Tyr Glu Gly Phe Pro Phe Val Gly Gly Leu

aag gcc atc gcc gaa tcg gcc acg gaa atc gcc gcg tac atc cgc gag 288  
Lys Ala Ile Ala Glu Ser Ala Thr Glu Ile Ala Ala Tyr Ile Arg Glu  
85 90 95

gtg aaa gaa aag acg ggc gcc gag aag att gag ctt gtc ggt cac tcc 336

## 21078WO.ST25.txt

Val Lys Glu Lys Thr Gly Ala Asp Lys Ile Asp Leu Val Gly His Ser			
100	105	110	
gaa ggc gcc ttc cag acc ctc tac gtc cct aag ttc gag gat ggt atc		384	
Glu Gly Ala Phe Gln Thr Leu Tyr Val Pro Lys Phe Glu Asp Gly Ile			
115	120	125	
tcg gag atg ctg gat aag ctg gtg gcc att gca cct ccc acc aga ggc		432	
Ser Glu Met Leu Asp Lys Leu Val Ala Ile Ala Pro Pro Thr Arg Gly			
130	135	140	
acc aac ttg gcg ggg atc tat gac atc gca tat gtt ctg gga aat cta		480	
Thr Asn Leu Ala Gly Ile Tyr Asp Ile Ala Tyr Val Leu Gly Asn Leu			
145	150	155	160
tcg cgc gat ctg ata ggc gac gtc ctg gat acc gtg ggc tgc gcc gcc		528	
Ser Arg Asp Leu Ile Gly Asp Val Leu Asp Thr Val Gly Cys Ala Ala			
165	170	175	
tgt gat gat ctg ggt ccg gat gga gca gcg att gac cgc ttg aac gat		576	
Cys Asp Asp Leu Gly Pro Asp Gly Ala Ala Ile Asp Arg Leu Asn Asp			
180	185	190	
ggc gag cct atc gtg cag ccg gga aat aat cta acg gtg att gca tcg		624	
Gly Glu Pro Ile Val Gln Pro Gly Asn Asn Leu Thr Val Ile Ala Ser			
195	200	205	
cgg tcc gac gaa ttg gtc acc cca acc acc acc tcc ttc gtg cat gaa		672	
Arg Ser Asp Glu Leu Val Thr Pro Thr Thr Ser Phe Val His Glu			
210	215	220	
gat ggg gtg acc aat gaa tgg gtg caa gac act tgt cct cta gac cct		720	
Asp Gly Val Thr Asn Glu Trp Val Gln Asp Thr Cys Pro Leu Asp Pro			
225	230	235	240
gtc ggt cat atc ggt gag gca tac gat ctg aac gtc tgg aat ttg gtc		768	
Val Gly His Ile Gly Glu Ala Tyr Asp Leu Asn Val Trp Asn Leu Val			
245	250	255	
aaa aac gcc ttg gac tct acg ccg aag cgt gag ttc gtc tgc tcg ctg		816	
Lys Asn Ala Leu Asp Ser Thr Pro Lys Arg Glu Phe Val Cys Ser Leu			
260	265	270	
gga tct ccc ggc agg tga		834	
Gly Ser Pro Gly Arg			
275			

&lt;210&gt; 15

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 15

Met Arg Leu Ser Ser Leu Ala Leu Ala Ser Ser Ala Ile Leu Pro Ala

## 21078WO.ST25.txt

1	5	10	15												
Leu	Gly	Tyr	Ser	Ile	Asn	Asp	Phe	Ser	Cys	Asn	Ser	Thr	Glu	His	Pro
		20			25										30
Asn	Pro	Val	Val	Leu	Leu	His	Gly	Leu	Gly	Ala	Thr	Tyr	Tyr	Glu	Asp
		35			40										45
Leu	Asn	Tyr	Leu	Gln	Gly	Trp	Leu	Gln	Gly	Tyr	Cys	Thr	Tyr		
		50			55										60
Ala	Lys	Thr	Tyr	Gly	Ala	Tyr	Glu	Gly	Phe	Pro	Phe	Val	Gly	Gly	Leu
	65		70			75									80
Lys	Ala	Ile	Ala	Glu	Ser	Ala	Thr	Glu	Ile	Ala	Ala	Tyr	Ile	Arg	Glu
		85			90										95
Val	Lys	Glu	Lys	Thr	Gly	Ala	Asp	Lys	Ile	Asp	Leu	Val	Gly	His	Ser
		100			105										110
Glu	Gly	Ala	Phe	Gln	Thr	Leu	Tyr	Val	Pro	Lys	Phe	Glu	Asp	Gly	Ile
	115			120			125								
Ser	Glu	Met	Leu	Asp	Lys	Leu	Val	Ala	Ile	Ala	Pro	Pro	Thr	Arg	Gly
		130			135										140
Thr	Asn	Leu	Ala	Gly	Ile	Tyr	Asp	Ile	Ala	Tyr	Val	Leu	Gly	Asn	Leu
	145			150			155								160
Ser	Arg	Asp	Leu	Ile	Gly	Asp	Val	Leu	Asp	Thr	Val	Gly	Cys	Ala	Ala
		165			170			175							
Cys	Asp	Asp	Leu	Gly	Pro	Asp	Gly	Ala	Ala	Ile	Asp	Arg	Leu	Asn	Asp
		180			185			190							
Gly	Glu	Pro	Ile	Val	Gln	Pro	Gly	Asn	Asn	Leu	Thr	Val	Ile	Ala	Ser
	195			200			205								
Arg	Ser	Asp	Glu	Leu	Val	Thr	Pro	Thr	Thr	Ser	Phe	Val	His	Glu	
	210			215			220								
Asp	Gly	Val	Thr	Asn	Glu	Trp	Val	Gln	Asp	Thr	Cys	Pro	Leu	Asp	Pro
	225			230			235								240
Val	Gly	His	Ile	Gly	Glu	Ala	Tyr	Asp	Leu	Asn	Val	Trp	Asn	Leu	Val
		245			250			255							
Lys	Asn	Ala	Leu	Asp	Ser	Thr	Pro	Lys	Arg	Glu	Phe	Val	Cys	Ser	Leu
		260			265			270							
Gly	Ser	Pro	Gly	Arg											
	275														

&lt;210&gt; 16

&lt;211&gt; 1881

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;400&gt; 16 .

ccgagtgtatc cgcgacttct gggtcagctt tggttctgcgg gctccaccag tgccgtcatc 60

## 21078WO.ST25.txt

gcacgcgaga	cccgccccgg	atgcttagct	gaagccggca	tagtccatcc	ccgctcgccc	120
gtgatgccca	acggtaactg	gaggagaggt	gcagggagga	tgccgttgca	tgaatcaagc	180
ccggggtttgc	actttcatcc	gctcgttcc	tactggcggg	ttcgccctct	ccatcgaagc	240
cacggatcct	tccatccgga	tcctggcaga	acagtggaga	agcagagctt	ggttatagta	300
gaaattatta	ataccgagct	ggtctgccc	tttttcccaa	accttccctc	tttccatccc	360
tctcgccctcg	cacccccc	atcctccctc	ccgccatgta	tatcccctcg	gtgctgcttc	420
tggccgcgag	cctgttccat	ggcgcaacgg	cgctgcccac	gcccggtc	acgcccacatcc	480
cgcccagcca	ggatccctgg	tacagtgcgc	ccgaggggctt	cgaggaggct	gatcccggtg	540
ccatcctcg	cgtcgccccc	gcccggca	acttgaccgt	ggtatgggc	aatgcgtcgg	600
cggcctacaa	catcctctac	cgcactacag	acagtcagta	caagccctcc	tgggctgtga	660
ccaccctgct	ggtgccccc	gtggccgcct	ccgcccgt	caaccagagt	gtcctgctct	720
cccaccagat	cgcctacgat	tcgttcgacg	tcaatgccag	tcccagctac	gccatgtaca	780
ccagccgc	ctccgatatt	atcctcgccc	tgcagcgcgg	ctggttcg	aacgtccccg	840
attacgaggg	ccccaatgcc	tcttcaccg	ccggtgtgca	gtccggccat	gccaccctcg	900
actcggtccg	cagcgtctc	gcctccggat	tcggcctgaa	cgaggacgc	cagtagctc	960
tgtgggtta	ctctggcggt	gccttgcca	gcgaatgggc	tgctgaactg	cagatgcaat	1020
acgctccga	gttgaacatt	gccggctgg	ccgtgggtgg	tctcactccc	aatgttacca	1080
gcgtcatgga	cacggtgacc	tcgaccatca	gtgcggact	catcccgcc	gccgcctgg	1140
gtctgtcg	ccagcacccc	gagacctacg	agttcatcct	cagccagctc	aagacgacgg	1200
gaccctacaa	ccgcacagga	ttcctagccg	ccaaggacct	gaccctgtcc	gaggcggagg	1260
tcttctacgc	cttccagaac	atttcgatt	actttgtcaa	cggatcgcc	acgttccagg	1320
cgagggtgg	gcagaaggcg	ctgaaccagg	acggatacat	gggctaccat	gggttcccgc	1380
agatgcccgt	gctcgctac	aaggctattc	acgatgagat	cagtccatc	caggatacgg	1440
atcgctgtat	caagcgctac	tgtggctgg	gattgaacat	cttgtatgag	cggaacacca	1500
tcggtgcca	ctcggcagag	caggtgaatg	gcaacgccc	ggcgtgaa	tggttgacga	1560
gcattttcga	cggaacgtat	gcmcagcagt	acaagaccga	gggggtgcacg	atccgcaatg	1620
tcactctgaa	cacgacttcc	tccgttatt	agagaggggg	ctgtgttat	gtgaataatg	1680
ctgaagatgg	ctgtgtatgg	acggtccgct	ctcctgtata	gtaatggct	aatgcatgcg	1740
gcttcatgaa	catggtacga	aagattagat	tatgtatata	gtgtggaa	gtaatgtatg	1800
atataatatc	tgtctatgat	ctatgttcc	gttattctat	acaaacgcga	ccattcacag	1860
aatgactact	ggcacatctg	c				1881

<210> 17  
<211> 1257  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(1257)

<400> 17  
atg tat atc ccc tcg gtg.ctg ctt ctg gcc gcg agc ctg ttc cat ggc

## 21078WO.ST25.txt

Met Tyr Ile Pro Ser Val Leu Leu Ala Ala Ser Leu Phe His Gly				
1	5	10	15	
gca acg gcg ctg ccc acg ccc ggc tcc acg ccc atc ccg ccc agc cag				96
Ala Thr Ala Leu Pro Thr Pro Gly Ser Thr Pro Ile Pro Pro Ser Gln				
20	25	30		
gat ccc tgg tac agt gcg ccc gag ggc ttc gag gag gct gat ccc ggt				144
Asp Pro Trp Tyr Ser Ala Pro Glu Gly Phe Glu Glu Ala Asp Pro Gly				
35	40	45		
gcc atc ctg cgc gtg cgcccccggccggccggccggccggccggccggccggccggcc				192
Ala Ile Leu Arg Val Arg Pro Ala Pro Gly Asn Leu Thr Val Val Val				
50	55	60		
ggc aat gcg tcg gcg gcc tac aac atc ctc tac cgc act aca gac agt				240
Gly Asn Ala Ser Ala Ala Tyr Asn Ile Leu Tyr Arg Thr Thr Asp Ser				
65	70	75	80	
cag tac aag ccc tcc tgg gct gtg acc acc ctg ctg gtg ccc ccc gtg				288
Gln Tyr Lys Pro Ser Trp Ala Val Thr Thr Leu Leu Val Pro Pro Val				
85	90	95		
gcc gcc tcc gcc gtc aac cag agt gtc ctg ctc tcc cac cag atc				336
Ala Ala Ser Ala Ala Val Asn Gln Ser Val Leu Leu Ser His Gln Ile				
100	105	110		
gcc tac gat tcg ttc gac gtc aat gcc agt ccc agc tac gcc atg tac				384
Ala Tyr Asp Ser Phe Asp Val Asn Ala Ser Pro Ser Tyr Ala Met Tyr				
115	120	125		
acc agc ccg ccc tcc gat att atc ctc gcc ctg cag cgc ggc tgg ttc				432
Thr Ser Pro Pro Ser Asp Ile Ile Leu Ala Leu Gln Arg Gly Trp Phe				
130	135	140		
gtt aac gtc ccc gat tac gag ggc ccc aat gcc tct ttc acc gcc ggt				480
Val Asn Val Pro Asp Tyr Glu Gly Pro Asn Ala Ser Phe Thr Ala Gly				
145	150	155	160	
gtg cag tcc ggc cat gcc acc ctc gac tcg gtc cgc agc gtg ctc gcc				528
Val Gln Ser Gly His Ala Thr Leu Asp Ser Val Arg Ser Val Leu Ala				
165	170	175		
tcc gga ttc ggc ctg aac gag gac gcc cag tac gct ctg tgg ggt tac				576
Ser Gly Phe Gly Leu Asn Glu Asp Ala Gln Tyr Ala Leu Trp Gly Tyr				
180	185	190		
tct ggc ggt gcc ttg gcc agc gaa tgg gct gct gaa ctg cag atg caa				624
Ser Gly Gly Ala Leu Ala Ser Glu Trp Ala Ala Glu Leu Gln Met Gln				
195	200	205		
tac gct ccc gag ttg aac att gcc ggt ctg gcc gtg ggt ggt ctc act				672
Tyr Ala Pro Glu Leu Asn Ile Ala Gly Leu Ala Val Gly Gly Leu Thr				
210	215	220		
ccc aat gtt acc agc gtc atg gac acg gtg acc tcg acc atc agt gcg				720
Pro Asn Val Thr Ser Val Met Asp Thr Val Thr Ser Thr Ile Ser Ala				
225	230	235	240	

## 21078WO.ST25.txt

gga ctc atc ccc gcc gcc ctg ggt ctg tcg agc cag cac ccc gag Gly Leu Ile Pro Ala Ala Ala Leu Gly Leu Ser Ser Gln His Pro Glu	768
245 250 255	
acc tac gag ttc atc ctc agc cag ctc aag acg acg gga ccc tac aac Thr Tyr Glu Phe Ile Leu Ser Gln Leu Lys Thr Thr Gly Pro Tyr Asn	816
260 265 270	
cgc aca gga ttc cta gcc gcc aag gac ctg acc ctg tcc gag gcg gag Arg Thr Gly Phe Leu Ala Ala Lys Asp Leu Thr Leu Ser Glu Ala Glu	864
275 280 285	
gtc ttc tac gcc ttc cag aac atc ttc gat tac ttt gtc aac gga tcg Val Phe Tyr Ala Phe Gln Asn Ile Phe Asp Tyr Phe Val Asn Gly Ser	912
290 295 300	
gcc acg ttc cag gcg gag gtg gtg cag aag gcg ctg aac cag gac gga Ala Thr Phe Gln Ala Glu Val Val Gln Lys Ala Leu Asn Gln Asp Gly	960
305 310 315 320	
tac atg ggc tac cat ggg ttc ccg cag atg ccg gtg ctc gcg tac aag Tyr Met Gly Tyr His Gly Phe Pro Gln Met Pro Val Leu Ala Tyr Lys	1008
325 330 335	
gct att cac gat gag atc agt ccc atc cag gat acg gat cgc gtg atc Ala Ile His Asp Glu Ile Ser Pro Ile Gln Asp Thr Asp Arg Val Ile	1056
340 345 350	
aag cgc tac tgt ggt ctg gga ttg aac atc ttg tat gag cgg aac acc Lys Arg Tyr Cys Gly Leu Gly Leu Asn Ile Leu Tyr Glu Arg Asn Thr	1104
355 360 365	
atc ggt ggc cac tcg gca gag cag gtg aat ggc aac gcc agg gcg tgg Ile Gly Gly His Ser Ala Glu Gln Val Asn Gly Asn Ala Arg Ala Trp	1152
370 375 380	
aac ttg ttg acg agc att ttc gac gga acg tat gcg cag cag tac aag Asn Trp Leu Thr Ser Ile Phe Asp Gly Thr Tyr Ala Gln Gln Tyr Lys	1200
385 390 395 400	
acc gag ggg tgc acg atc cgc aat gtc act ctg aac acg act tcc tcc Thr Glu Gly Cys Thr Ile Arg Asn Val Thr Leu Asn Thr Thr Ser Ser	1248
405 410 415	
gtt tat tag Val Tyr	1257

&lt;210&gt; 18

&lt;211&gt; 418

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 18

Met Tyr Ile Pro Ser Val Leu Leu Leu Ala Ala Ser Leu Phe His Gly

## 21078WO.ST25.txt

1	5	10	15
Ala	Thr Ala	Leu Pro Thr Pro Gly Ser Thr Pro Ile Pro Pro Ser Gln	
	20	25	30
Asp	Pro Trp Tyr Ser Ala Pro Glu Gly Phe Glu Glu Ala Asp Pro Gly		
	35	40	45
Ala	Ile Leu Arg Val Arg Pro Ala Pro Gly Asn Leu Thr Val Val Val		
	50	55	60
Gly	Asn Ala Ser Ala Ala Tyr Asn Ile Leu Tyr Arg Thr Thr Asp Ser		
	65	70	75
60	75	80	
Gln	Tyr Lys Pro Ser Trp Ala Val Thr Thr Leu Leu Val Pro Pro Val		
	85	90	95
Ala	Ala Ser Ala Ala Val Asn Gln Ser Val Leu Leu Ser His Gln Ile		
	100	105	110
Ala	Tyr Asp Ser Phe Asp Val Asn Ala Ser Pro Ser Tyr Ala Met Tyr		
	115	120	125
Thr	Ser Pro Pro Ser Asp Ile Ile Leu Ala Leu Gln Arg Gly Trp Phe		
	130	135	140
Val	Asn Val Pro Asp Tyr Glu Gly Pro Asn Ala Ser Phe Thr Ala Gly		
	145	150	155
160	155	160	
Val	Gln Ser Gly His Ala Thr Leu Asp Ser Val Arg Ser Val Leu Ala		
	165	170	175
Ser	Gly Phe Gly Leu Asn Glu Asp Ala Gln Tyr Ala Leu Trp Gly Tyr		
	180	185	190
Ser	Gly Gly Ala Leu Ala Ser Glu Trp Ala Ala Glu Leu Gln Met Gln		
	195	200	205
Tyr	Ala Pro Glu Leu Asn Ile Ala Gly Leu Ala Val Gly Gly Leu Thr		
	210	215	220
Pro	Asn Val Thr Ser Val Met Asp Thr Val Thr Ser Thr Ile Ser Ala		
	225	230	235
240	235	240	
Gly	Leu Ile Pro Ala Ala Ala Leu Gly Leu Ser Ser Gln His Pro Glu		
	245	250	255
Thr	Tyr Glu Phe Ile Leu Ser Gln Leu Lys Thr Thr Gly Pro Tyr Asn		
	260	265	270
Arg	Thr Gly Phe Leu Ala Ala Lys Asp Leu Thr Leu Ser Glu Ala Glu		
	275	280	285
Val	Phe Tyr Ala Phe Gln Asn Ile Phe Asp Tyr Phe Val Asn Gly Ser		
	290	295	300
Ala	Thr Phe Gln Ala Glu Val Val Gln Lys Ala Leu Asn Gln Asp Gly		
	305	310	315
320	315	320	
Tyr	Met Gly Tyr His Gly Phe Pro Gln Met Pro Val Leu Ala Tyr Lys		
	325	330	335
Ala	Ile His Asp Glu Ile Ser Pro Ile Gln Asp Thr Asp Arg Val Ile		
	340	345	350
Lys	Arg Tyr Cys Gly Leu Gly Leu Asn Ile Leu Tyr Glu Arg Asn Thr		

## 21078WO.ST25.txt

355	360	365
Ile Gly Gly His Ser Ala Glu Gln Val Asn Gly Asn Ala Arg Ala Trp		
370	375	380
Asn Trp Leu Thr Ser Ile Phe Asp Gly Thr Tyr Ala Gln Gln Tyr Lys		
385	390	395
Thr Glu Gly Cys Thr Ile Arg Asn Val Thr Leu Asn Thr Thr Ser Ser		400
405	410	415
Val Tyr		

&lt;210&gt; 19

&lt;211&gt; 2809

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;400&gt; 19

agtaatgtat catttcaaag atcagtaaat gaaatctgct gcacaatgca cgctttgaga	60
acgacgatgc gaatcgtaga atgcccagt cagtctgcgt ggtcagacga gaccatata	120
ttgcataatgt acaatcttagt agtataatat ggtgtaaatc cccataacct gataactata	180
cacactatca gggcttgggt acatgagcga agtagtccca acaatcaaac aatcatccaa	240
actccaagcc aaatgccagc gaaaacaaca aaagcacaaac atgatgttac agtgcactag	300
ggaaaccaat ctgtgtcacc atcactcagg acaccagata taacgaaccc ccctcacaga	360
ccacgagtct tctccggatc catctgcacc tcatacaccgc taatttcctt gaccgtctca	420
aacgcccgt tgccgcata tagctctgg gacgagctgg agccgcgc ttccgtcgtc	480
gataccgaga tgggctggtt tccgcggAAC cgcttgcgc tatcgatcag gccgcgtcta	540
tagaaggaca aacagtttagt aaccctgtatg acttggcggt gattgcgttt tacaagaagg	600
tagcggctct ttactcaattt gcactcgctg aatcccttcc gcaattgctg gcatcgatg	660
ggaagctcgt cgacgtacgg ctcactcaga cattcgcggg gcgagcgcgg ttgcaccatg	720
atgcagtcgt attcttggag acattggcc agagcatttc ctgttcatcc aggtgagatt	780
gattagagag tggggagctg aagctgaagt tggggacaat gaggtggta tctccgttcg	840
gggatacgtc gagtatccaa gcccgaattt aagagtatgg taaaggatata aagggtcaaa	900
cgtactgatc tcttggcagg aactcggcat tttggcgaac aacaatggcc gaattgctca	960
gccaactgac aagcaggaac aataccggc tgccgcggcg gacatctgg gataatttgt	1020
ctgatcgaa aacaaactca accaacgggc cttgccccgg attaggtaa ccatcacatg	1080
aagaaggccc ccatgacgtc tgggggaat cctgacttgc tgcttgcattt gcttgattt	1140
tcctcttccc ctatgtatgc ggtcttgggt ctttgaagca ttgttgcgc gcattatgg	1200
tcactactac tactgcaggat gataagtatt ttagttgggt gatttgcataa ttgtccatcc	1260
cttttgcata ataggaggat tggcttaat cgtcatggcg cgcttccgg tcattggacg	1320
gctgtttgg ttcgaggatt tggcccttt tgggtcgctg attttggat tgctggatg	1380
ggttatacat attatcacat tctgtctgcg taagtagtgt gttcatttctc tggaaattgt	1440
gtctatgtcg agggcaaga gctaactgac gcagctgaac ctgttattaa gttctgttac	1500
gatcgatcca agactatctt caacgccttc attcctccc atgacccggc taagcgcgg	1560
aaagaagaga aaattgctgc gtccgttgct ctggcgtcgg acttcacggta tataatgcgcg	1620
ctgttccggat atgaggcggg ggaacatatac gtccagacag gggatggcta tctgcttgcgt	1680

## 21078WO.ST25.txt

ctgcaccgac	tgccctatcg	gaaaggagag	gaggggagga	agatcaacca	gggcgaaggg	1740
agcatcaaga	agaaggtcgt	ctatctccac	catgtctca	tgatgtgcag	tgaagtctgg	1800
atctgtctgt	cagaggagca	gcatgcctt	ccgttcaat	tagtcgaaag	gggctatgac	1860
gtgtggttgg	ggaacaatacg	aggaaacaag	tactcgaaga	agtccgtcaa	gcattcgccc	1920
ctgtcgaacg	agttctggga	ctttcgatc	gatcagttct	cgttccatga	tatcccagac	1980
agcatcaagt	atatcctgga	agtgacaggg	cagccctccc	tgtcatacgt	ggggttctcg	2040
cagggAACAG	cgcaggcatt	tgcgacgctg	tccattcatc	ctttgttcaa	tcagaagatc	2100
gatgtctttg	tgctctcgc	gccggcaatg	gctccgacag	gtcttccaaa	tcatctcgtg	2160
gactcgctca	tgaaggcttc	gccgaacttc	ctgtttctgc	tgtttggcag	acgcagcatc	2220
cttagctcaa	cgacgatgtg	gcagacaatt	ctctaccgc	ctatctttgt	ttggatcatc	2280
gacacgtcac	ttcgcggcct	gttcaattgg	aggtgcaaga	acatcagccg	ctggcagaag	2340
ctggcagggt	acctgcattc	gttttcttc	actagcacca	agtcggcgt	ccattggttc	2400
cagattattc	ggcacccgaa	tttccagttc	tacgatgacg	aaatccatgc	cccgctcagt	2460
atttgtggcca	gtgagcgtt	ttacaagccg	gtcaagtacc	cgactaagaa	cattaagacg	2520
ccattgtcc	tgttgtatgg	cgttagcgat	agtctcggt	atataaacgt	gatgttgc	2580
gagctccctc	gccccggcgt	ggcgaaggaa	atcccgagt	atgagcattt	agatttcttgc	2640
tggcgcgtg	atgtggacca	attggatttc	aaccatgtct	tcgaagcgt	ggagcgtac	2700
agctcgagaa	atcagaaagg	gacattgatg	gagaaggta	atggtgccgc	gggcacatata	2760
gtaccgacat	aaagtacgag	gtcctgcacc	aatgaagaca	cgcataatc		2809

&lt;210&gt; 20

&lt;211&gt; 1413

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1413)

&lt;400&gt; 20

atg	gcg	cgc	gtt	ccg	gtc	att	gga	cgg	ctg	ttt	tgg	ttc	gag	tat	ttg		48
Met	Ala	Arg	Val	Pro	Val	Ile	Gly	Arg	Leu	Phe	Trp	Phe	Glu	Tyr	Leu		
1																	
5																	
10																	
15																	
gcc	ctt	ttt	ggg	tcg	ctg	att	ttg	gta	ttg	ctg	gaa	tgg	gtt	ata	cat		96
Ala	Leu	Phe	Gly	Ser	Leu	Ile	Leu	Val	Leu	Leu	Glu	Trp	Val	Ile	His		
20																	
25																	
30																	
att	atc	aca	ttc	tgt	ctg	cct	gaa	cct	gtt	att	aag	ttc	tgt	tac	gat		144
Ile	Ile	Thr	Phe	Cys	Leu	Pro	Glu	Pro	Val	Ile	Lys	Phe	Cys	Tyr	Asp		
35																	
40																	
45																	
cga	tcc	aag	act	atc	ttc	aac	gcc	ttc	att	cct	ccc	gat	gac	ccg	gct		192
Arg	Ser	Lys	Thr	Ile	Phe	Asn	Ala	Phe	Ile	Pro	Pro	Asp	Asp	Pro	Ala		
50																	
55																	
60																	
aag	cgc	ggt	aaa	gaa	gag	aaa	att	gct	gcg	tcg	gtt	gct	ctg	gcg	tcg		240

## 21078WO.ST25.txt

Lys Arg Gly Lys Glu Glu Lys Ile Ala Ala Ser Val Ala Leu Ala Ser			
65	70	75	80
gac ttc acg gat ata tgc gcg ctg ttc gga tat gag gcg gag gaa cat			288
Asp Phe Thr Asp Ile Cys Ala Leu Phe Gly Tyr Glu Ala Glu Glu His			
85	90	95	
atc gtc cag aca ggg gat ggc tat ctg ctt ggt ctg cac cga ctg ccc			336
Ile Val Gln Thr Gly Asp Gly Tyr Leu Leu Gly Leu His Arg Leu Pro			
100	105	110	
tat cgg aaa gga gag gag ggg agg aag atc aac cag ggc gaa ggg agc			384
Tyr Arg Lys Gly Glu Gly Arg Lys Ile Asn Gln Gly Glu Gly Ser			
115	120	125	
atc aag aag aag gtc gtc tat ctc cac cat ggt ctc atg atg tgc agt			432
Ile Lys Lys Val Val Tyr Leu His His Gly Leu Met Met Cys Ser			
130	135	140	
gaa gtc tgg atc tgt ctg tca gag gag cag cga tgc ctt ccg ttt caa			480
Glu Val Trp Ile Cys Leu Ser Glu Glu Gln Arg Cys Leu Pro Phe Gln			
145	150	155	160
tta gtc gaa agg ggc tat gac gtg tgg ttg ggg aac aat aga gga aac			528
Leu Val Glu Arg Gly Tyr Asp Val Trp Leu Gly Asn Asn Arg Gly Asn			
165	170	175	
aag tac tcg aag aag tcc gtc aag cat tcg ccc ctg tcg aac gag ttc			576
Lys Tyr Ser Lys Ser Val Lys His Ser Pro Leu Ser Asn Glu Phe			
180	185	190	
tgg gac ttt tcg atc gat cag ttc tcg ttc cat gat atc cca gac agc			624
Trp Asp Phe Ser Ile Asp Gln Phe Ser Phe His Asp Ile Pro Asp Ser			
195	200	205	
atc aag tat atc ctg gaa gtg aca ggg cag ccc tcc ctg tca tac gtg			672
Ile Lys Tyr Ile Leu Glu Val Thr Gly Gln Pro Ser Leu Ser Tyr Val			
210	215	220	
ggg ttc tcg cag gga aca gcg cag gca ttt gcg acg ctg tcc att cat			720
Gly Phe Ser Gln Gly Thr Ala Gln Ala Phe Ala Thr Leu Ser Ile His			
225	230	235	240
cct ttg ttg aat cag aag atc gat gtc ttt gtg gct ctc gcg ccg gca			768
Pro Leu Leu Asn Gln Lys Ile Asp Val Phe Val Ala Leu Ala Pro Ala			
245	250	255	
atg gct ccg aca ggt ctt cca aat cat ctc gtg gac tcg ctc atg aag			816
Met Ala Pro Thr Gly Leu Pro Asn His Leu Val Asp Ser Leu Met Lys			
260	265	270	
gct tcg ccg aac ttc ctg ttt ctg ctg ttt ggc aga cgc agc atc ctt			864
Ala Ser Pro Asn Phe Leu Phe Leu Leu Phe Gly Arg Arg Ser Ile Leu			
275	280	285	
agc tca acg acg atg tgg cag aca att ctc tac ccg cct atc ttt gtt			912
Ser Ser Thr Thr Met Trp Gln Thr Ile Leu Tyr Pro Pro Ile Phe Val			
290	295	300	

21078W0.ST25.txt

tgg atc atc gac acg tca ctt cgc ggc ctg ttc aat tgg agg tgc aag		960
Trp Ile Ile Asp Thr Ser Leu Arg Gly Leu Phe Asn Trp Arg Cys Lys		
305 310 315 320		
aac atc agc cgc tgg cag aag ctg gca ggg tac ctg cat ctg ttt tcc		1008
Asn Ile Ser Arg Trp Gln Lys Leu Ala Gly Tyr Leu His Leu Phe Ser		
325 330 335		
ttc act agc acc aag tcg gtc cat tgg ttc cag att att cggt cac		1056
Phe Thr Ser Thr Lys Ser Val Val His Trp Phe Gln Ile Ile Arg His		
340 345 350		
cggt aat ttc cag ttc tac gat gac gaa atc cat gcc ccgt ctc agt att		1104
Arg Asn Phe Gln Phe Tyr Asp Asp Glu Ile His Ala Pro Leu Ser Ile		
355 360 365		
gtg gcc agt gag cga ttt tac aag ccgt gtc aag tac ccgt act aag aac		1152
Val Ala Ser Glu Arg Phe Tyr Lys Pro Val Lys Tyr Pro Thr Lys Asn		
370 375 380		
att aag acg ccc att gtc ctg ttg tat ggc ggt agc gat agt ctc gtt		1200
Ile Lys Thr Pro Ile Val Leu Leu Tyr Gly Gly Ser Asp Ser Leu Val		
385 390 395 400		
gat atc aac gtg atg ttg tcc gag ctc cct cgc ggg acc gtg gcg aag		1248
Asp Ile Asn Val Met Leu Ser Glu Leu Pro Arg Gly Thr Val Ala Lys		
405 410 415		
gaa atc ccgt cag tat gag cat tta gat ttc ttg tgg gcg cgt gat gtg		1296
Glu Ile Pro Gln Tyr Glu His Leu Asp Phe Leu Trp Ala Arg Asp Val		
420 425 430		
gac caa ttg gta ttc aac cat gtc ttc gaa gcg ctg gag cgg tac agc		1344
Asp Gln Leu Val Phe Asn His Val Phe Glu Ala Leu Glu Arg Tyr Ser		
435 440 445		
tcg gag aat cag aaa ggg aca ttg atg gag aag gtt aat ggt gcc gcg		1392
Ser Glu Asn Gln Lys Gly Thr Leu Met Glu Lys Val Asn Gly Ala Ala		
450 455 460		
ggc aca tat gta ccgt aca taa		1413
Gly Thr Tyr Val Pro Thr		
465 470		

<210> 21

<211> 470

<212> PRT

<213> Aspergillus niger

<400> 21

Met	Ala	Arg	Val	Pro	Val	Ile	Gly	Arg	Leu	Phe	Trp	Phe	Glu	Tyr	Leu
1				5	.	.			10				15		
Ala	Leu	Phe	Gly	Ser	Leu	Ile	Leu	Val	Leu	Leu	Glu	Trp	Val	Ile	His

## 21078WO.ST25.txt

20	25	30
Ile Ile Thr Phe Cys Leu Pro Glu Pro Val Ile Lys Phe Cys Tyr Asp		
35	40	45
Arg Ser Lys Thr Ile Phe Asn Ala Phe Ile Pro Pro Asp Asp Pro Ala		
50	55	60
Lys Arg Gly Lys Glu Glu Lys Ile Ala Ala Ser Val Ala Leu Ala Ser		
65	70	75
Asp Phe Thr Asp Ile Cys Ala Leu Phe Gly Tyr Glu Ala Glu Glu His		
85	90	95
Ile Val Gln Thr Gly Asp Gly Tyr Leu Leu Gly Leu His Arg Leu Pro		
100	105	110
Tyr Arg Lys Gly Glu Glu Gly Arg Lys Ile Asn Gln Gly Glu Gly Ser		
115	120	125
Ile Lys Lys Val Val Tyr Leu His His Gly Leu Met Met Cys Ser		
130	135	140
Glu Val Trp Ile Cys Leu Ser Glu Glu Gln Arg Cys Leu Pro Phe Gln		
145	150	155
Leu Val Glu Arg Gly Tyr Asp Val Trp Leu Gly Asn Asn Arg Gly Asn		
165	170	175
Lys Tyr Ser Lys Lys Ser Val Lys His Ser Pro Leu Ser Asn Glu Phe		
180	185	190
Trp Asp Phe Ser Ile Asp Gln Phe Ser Phe His Asp Ile Pro Asp Ser		
195	200	205
Ile Lys Tyr Ile Leu Glu Val Thr Gly Gln Pro Ser Leu Ser Tyr Val		
210	215	220
Gly Phe Ser Gln Gly Thr Ala Gln Ala Phe Ala Thr Leu Ser Ile His		
225	230	235
Pro Leu Leu Asn Gln Lys Ile Asp Val Phe Val Ala Leu Ala Pro Ala		
245	250	255
Met Ala Pro Thr Gly Leu Pro Asn His Leu Val Asp Ser Leu Met Lys		
260	265	270
Ala Ser Pro Asn Phe Leu Phe Leu Leu Phe Gly Arg Arg Ser Ile Leu		
275	280	285
Ser Ser Thr Thr Met Trp Gln Thr Ile Leu Tyr Pro Pro Ile Phe Val		
290	295	300
Trp Ile Ile Asp Thr Ser Leu Arg Gly Leu Phe Asn Trp Arg Cys Lys		
305	310	315
Asn Ile Ser Arg Trp Gln Lys Leu Ala Gly Tyr Leu His Leu Phe Ser		
325	330	335
Phe Thr Ser Thr Lys Ser Val Val His Trp Phe Gln Ile Ile Arg His		
340	345	350
Arg Asn Phe Gln Phe Tyr Asp Asp Glu Ile His Ala Pro Leu Ser Ile		
355	360	365
Val Ala Ser Glu Arg Phe Tyr Lys Pro Val Lys Tyr Pro Thr Lys Asn		

## 21078WO.ST25.txt

370	375	380
Ile Lys Thr Pro Ile Val Leu Leu Tyr Gly Gly Ser Asp Ser Leu Val		
385	390	395
Asp Ile Asn Val Met Leu Ser Glu Leu Pro Arg Gly Thr Val Ala Lys		400
405	410	415
Glu Ile Pro Gln Tyr Glu His Leu Asp Phe Leu Trp Ala Arg Asp Val		
420	425	430
Asp Gln Leu Val Phe Asn His Val Phe Glu Ala Leu Glu Arg Tyr Ser		
435	440	445
Ser Glu Asn Gln Lys Gly Thr Leu Met Glu Lys Val Asn Gly Ala Ala		
450	455	460
Gly Thr Tyr Val Pro Thr		
465	470	

&lt;210&gt; 22

&lt;211&gt; 3328

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;400&gt; 22

gatttatgaa	gacaggggag	ctctcagtag	atgatcttcg	cacaattgca	cttccttggg	60
agcctgtta	gtctctagtg	aattattgtat	agacaggta	tctgcctcg	gggggttcta	120
ctaacaacgt	gatatctatg	ttgctccctt	actttagaag	aaagggtctg	cttggtagct	180
ggaaccagt	atatagttg	tgtgagttata	tgaagattcc	aatgctttgg	aatattccgc	240
cgtggctgaa	tgtatggact	ctcaactgcc	agccaaggga	ttcctcccg	aatttttgca	300
catatgttgt	tgtatgcctt	tccctctggc	attcaactgt	tgctgcctcg	ggtgggaccc	360
gacagtcc	aaacgatgaa	atcttattgg	ctctgctagt	ttagctcggt	ttcaccattt	420
ctattggcgc	tttctcactc	tactccatat	tacagcttcc	gctttgcaat	gcggggctgt	480
gctgcgactt	tgaattgctc	gcatagcaag	agacactgac	cagcaatcca	gctttctgc	540
ccacatatgt	tgcctttgcc	tttagtatctc	ataattttatg	tgtccagtga	gacagtttgt	600
ttgtactgta	gcttgagttt	ggaatcgtgt	cctgtgacca	tggaaatata	tattctggat	660
ctcagaacat	ctctaccgtt	tgtaattttt	gatatacttc	ccaggatggg	acaatggga	720
cgatgagttat	tgggatgcca	tatcaactga	aagccttta	gacagactgc	acctattttt	780
attatgctaa	attctttacg	agacactttc	ttcaagtttc	tggccctttg	tgaggcagag	840
tgaaaacacga	gcgttcaaac	ttgtgttgta	gatgtttatg	atatttatct	cagacagtct	900
ttcccacatcc	tgtatcccc	aacagaaaaaa	gatacacagt	atatcaactag	aagctcccaa	960
tagttatcat	gctgcaccct	aacagcaatg	cagtcaccct	gctgcgtcag	cgaccggat	1020
tccggagaag	tatccgagat	agcgataagg	atgcggagat	aagattggca	agtggagatg	1080
agaaaagat	cctcggcctc	agaagttaggc	ccgatgataa	ataactagtg	aacaagtccc	1140
ccgcccctct	ccgagcaaac	tacacttcaa	catgctgaat	gcacgctcca	ttgctctggc	1200
ctcggtgcc	gttcttctcc	tactattcgc	ccagcaactt	gcctctcacc	caaccgagca	1260
gattcaagcc	attctggctc	cgtgggtccc	ggccgcacta	caagatgtcg	tgctctataa	1320
tcgacctcgc	gtcataatcc	cccaggcac	tgtcgtcggc	acgacattga	cagacacgct	1380

## 21078WO.ST25.txt

caagtccccg	gtagatgctt	tccgaggaat	tccatacgca	ttgcctccaa	ttggggatag	1440
acggttcgc	cgtgcggagg	ctgtccatgc	gacggacgag	attatcgatg	ctagtgaatt	1500
cggcccaagg	tatgcttctt	atacgacatt	cagatcatat	ctgaccttc	agggccctg	1560
gaaagcagct	cttgaatcca	aatgacatag	gtggtgatga	agactgtctc	acagtcaatg	1620
tcttccggcc	tcatggcgct	cagggaaaac	tccctgtcgc	tgtatacgtg	cacggcggag	1680
cctacaatcg	cggcacttgt	aggtgtatca	ccctcagttcc	tctatatacc	cacagctaaa	1740
tatccagcct	ccggacacaa	cacggcctcg	atggtcggct	ggtcgacga	gcccttcgtt	1800
gcagtcagct	tcaactaccg	gtacgtcctc	aaacctgtcc	tccgaatcaa	ctcaactaac	1860
aacccatcag	catcggcgcc	ctcggcttcc	tcccatccac	cctaaccgcc	aaagaaggaa	1920
tcctcaacct	aggcctccat	gaccagatcc	tcctgctgca	atgggtccaa	gaaaacatcg	1980
cacatttcaa	cggcgaccca	acccaagtca	ctctaattcg	cctctccgccc	ggcgcgact	2040
ccgtatgccc	ccttctaaga	tacaaataga	actcagtccc	ctaccccaa	actaacgcca	2100
cacagatagc	ccaccacatc	atgaactaca	acccacccaa	caccccccctc	tttcaccgcg	2160
ccatcatcga	atccggcgcc	gccacccccc	gcccgtcca	cccctacaac	gcctccctcc	2220
acgaatccca	attcacagac	ttcctactg	aaacgggctg	actaacctc	cccgacactg	2280
ccatttgcc	ctgtctccgc	gccctccat	cctcagccat	taccaccgc	tccatctccg	2340
tcttcgacaa	atacaacccc	tccatccgct	gggccttcca	acccgtcatc	gaccacgaga	2400
tcatccaccc	ccggcccatc	gacgcctggc	gctcaggaaa	gtgaaatagg	atgcccattcc	2460
taacgggctt	caactcgaac	gagggacat	actacgtccc	tcgcaacctc	tctctctccg	2520
aggatttcac	ttcggttctt	cgaacccctcc	tcccccgcgt	ccccgagagc	gacatccaga	2580
ccatcgatga	gatctacccc	gatccgaatg	tatatgtac	ggcgtcgcca	tacctcgaga	2640
caaggccat	cccgagtcta	ggaaggcagt	ttaagcgct	ggaggcggcg	tatgggcatt	2700
atgcgtatgc	gtgtccagta	cggcagacgg	cggggtttgc	tgctaattgt	gatggttgtg	2760
gtgagccggt	gtttttgtat	cgctggcggt	tgaataagac	tgttatttgg	ggcgcgaacc	2820
atggtgatca	gatggagtat	gagacgttta	atcctgcgtt	tagggatatt	tcggaggctc	2880
agagggaggt	tgccgggttg	tttcatgcgt	atgtgacttc	gtttgtggtg	catggggatc	2940
cgaatttct	ggggggtagg	tatgagggga	gggaggtttg	ggagaggtat	agtggggagg	3000
gaggggaggt	gatgggtttt	ggggagggga	atgatgaacg	tgctgggggg	gatggagttg	3060
gggttgcggc	gaggttgaag	agggatgagt	ggggggtgaa	ggagtgtgga	ttttggcttg	3120
ggaggagtgg	gattcccgag	tgtatggttt	tttatataata	gtcttagtgg	aggggatgt	3180
tataactgtag	tcaactatctg	tagaacttta	cttggtggt	agatagtaaa	tactacaact	3240
gctgaagacc	ttgggataga	acgacatgct	gtttaatcct	caaccctgac	tagatatatt	3300
gtgcattact	tgcattccacg	cctaacat				3328

&lt;210&gt; 23

&lt;211&gt; 1779

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1779)

## 21078WO.ST25.txt

&lt;400&gt; 23

atg ctg aat gca cgc tcc att gct ctg gcc tcg ttg cca gtt ctt ctc Met Leu Asn Ala Arg Ser Ile Ala Leu Ala Ser Leu Pro Val Leu Leu	48
1 5 10 15	
cta cta ttc gcc cag caa ctt gcc tct cac cca acc gag cag att caa Leu Leu Phe Ala Gln Gln Leu Ala Ser His Pro Thr Glu Gln Ile Gln	96
20 25 30	
gcc att ctg gct ccg tgg gtc ccg gcc gca cta caa gat gtc gtg ctc Ala Ile Leu Ala Pro Trp Val Pro Ala Ala Leu Gln Asp Val Val Leu	144
35 40 45	
tat aat cga cct cgc gtc ata atc ccc cag ggc act gtc gtc ggc acg Tyr Asn Arg Pro Arg Val Ile Ile Pro Gln Gly Thr Val Val Gly Thr	192
50 55 60	
acc ttg aca gac acg ctc aag tcc ccg gta gat gct ttc cga gga att Thr Leu Thr Asp Thr Leu Lys Ser Pro Val Asp Ala Phe Arg Gly Ile	240
65 70 75 80	
cca tac gca ttg cct cca att ggg gat aga cgg ttt cgc cgt gcg gag Pro Tyr Ala Leu Pro Pro Ile Gly Asp Arg Arg Phe Arg Arg Ala Glu	288
85 90 95	
gct gtc cat gcg acg gac gag att atc gat gct agt gaa ttc ggc cca Ala Val His Ala Thr Asp Glu Ile Ile Asp Ala Ser Glu Phe Gly Pro	336
100 105 110	
agg tgc cct gga aag cag ctc ttg aat cca aat gac ata ggt ggt gat Arg Cys Pro Gly Lys Gln Leu Leu Asn Pro Asn Asp Ile Gly Gly Asp	384
115 120 125	
gaa gac tgt ctc aca gtc aat gtc ttc cgg cct cat ggc gct cag gga Glu Asp Cys Leu Thr Val Asn Val Phe Arg Pro His Gly Ala Gln Gly	432
130 135 140	
aaa ctc cct gtc gct gta tac gtg cac ggc gga gcc tac aat cgc ggc Lys Leu Pro Val Ala Val Tyr Val His Gly Gly Ala Tyr Asn Arg Gly	480
145 150 155 160	
act gct aaa tat cca gcc tcc gga cac aac acg gcc tcg atg gtc ggc Thr Ala Lys Tyr Pro Ala Ser Gly His Asn Thr Ala Ser Met Val Gly	528
165 170 175	
tgg tcg gac gag ccc ttc gtt gca gtc agc ttc aac tac cgc atc ggc Trp Ser Asp Glu Pro Phe Val Ala Val Ser Phe Asn Tyr Arg Ile Gly	576
180 185 190	
gcc ctc ggc ttc ctc cca tcc acc cta acc gcc aaa gaa gga atc ctc Ala Leu Gly Phe Leu Pro Ser Thr Leu Thr Ala Lys Glu Gly Ile Leu	624
195 200 205	
aac cta ggc ctc cat gac cag atc ctc ctg cta tgg gtc caa gaa Asn Leu Gly Leu His Asp Gln Ile Leu Leu Gln Trp Val Gln Glu	672
210 215 220	
aac atc gca cat ttc aac ggc gac cca acc caa gtc act cta atc ggc	720

## 21078WO.ST25.txt

Asn Ile Ala His Phe Asn Gly Asp Pro Thr Gln Val Thr Leu Ile Gly			
225	230	235	240
ctc tcc gcc ggc gcg cac tcc ata gcc cac cac atc atg aac tac aac			768
Leu Ser Ala Gly Ala His Ser Ile Ala His His Ile Met Asn Tyr Asn			
245	250	255	
cca cca aac acc ccc ctc ttt cac cgc gcc atc atc gaa tcc ggc gcc			816
Pro Pro Asn Thr Pro Leu Phe His Arg Ala Ile Ile Glu Ser Gly Ala			
260	265	270	
gcc acc tcc cgc gcc gtc cac ccc tac aac gcc tcc ctc cac gaa tcc			864
Ala Thr Ser Arg Ala Val His Pro Tyr Asn Ala Ser Leu His Glu Ser			
275	280	285	
caa ttc aca gac ttc ctc act gaa acg ggc tgc act aac ctc ccc gac			912
Gln Phe Thr Asp Phe Leu Thr Glu Thr Gly Cys Thr Asn Leu Pro Asp			
290	295	300	
act gcc att ttg ccc tgt ctc cgc gcc ctc cca tcc tca gcc att acc			960
Thr Ala Ile Leu Pro Cys Leu Arg Ala Leu Pro Ser Ser Ala Ile Thr			
305	310	315	320
acc gcc tcc atc tcc gtc ttc gac aaa tac aac ccc tcc atc cgc tgg			1008
Thr Ala Ser Ile Ser Val Phe Asp Lys Tyr Asn Pro Ser Ile Arg Trp			
325	330	335	
gcc ttc caa ccc gtc atc gac cac gag atc atc cac cgc cgccccc atc			1056
Ala Phe Gln Pro Val Ile Asp His Glu Ile Ile His Arg Arg Pro Ile			
340	345	350	
gac gcc tgg cgc tca gga aag tgg aat agg atg ccc atc cta acg ggc			1104
Asp Ala Trp Arg Ser Gly Lys Trp Asn Arg Met Pro Ile Leu Thr Gly			
355	360	365	
ttc aac tcg aac gag ggg aca tac tac gtc cct cgc aac ctc tct ctc			1152
Phe Asn Ser Asn Glu Gly Thr Tyr Tyr Val Pro Arg Asn Leu Ser Leu			
370	375	380	
tcc gag gat ttc act tcg ttc ttc cga acc ctc ctc ccc gcg tac ccc			1200
Ser Glu Asp Phe Thr Ser Phe Phe Arg Thr Leu Leu Pro Ala Tyr Pro			
385	390	395	400
gag agc gac atc cag acc atc gat gag atc tac ccc gat ccg aat gta			1248
Glu Ser Asp Ile Gln Thr Ile Asp Glu Ile Tyr Pro Asp Pro Asn Val			
405	410	415	
tat gct acg gcg tcg cca tac ctc gag aca agg ccg atc ccg agt cta			1296
Tyr Ala Thr Ala Ser Pro Tyr Leu Glu Thr Arg Pro Ile Pro Ser Leu			
420	425	430	
gga agg cag ttt aag cgg ctg gag gcg gcg tat ggg cat tat gcg tat			1344
Gly Arg Gln Phe Lys Arg Leu Glu Ala Ala Tyr Gly His Tyr Ala Tyr			
435	440	445	
gcg tgt cca gta cgg cag acg gcg ggg ttt gtt gct aat gat gat ggt			1392
Ala Cys Pro Val Arg Gln Thr Ala Gly Phe Val Ala Asn Asp Asp Gly			
450	455	460	

## 21078WO.ST25.txt

tgt ggt gag ccg gtg ttt ttg tat cgc tgg gcg ttg aat aag act gtt		1440
Cys Gly Glu Pro Val Phe Leu Tyr Arg Trp Ala Leu Asn Lys Thr Val		
465 470 475 480		
att gga ggc gcg aac cat ggt gat cag atg gag tat gag acg ttt aat		1488
Ile Gly Gly Ala Asn His Gly Asp Gln Met Glu Tyr Glu Thr Phe Asn		
485 490 495		
cct gcg gtt agg gat att tcg gag gct cag agg gag gtt gcg ggg ttg		1536
Pro Ala Val Arg Asp Ile Ser Glu Ala Gln Arg Glu Val Ala Gly Leu		
500 505 510		
ttt cat gcg tat gtg act tcg ttt gtg gtg cat ggg gat ccg aat gtt		1584
Phe His Ala Tyr Val Thr Ser Phe Val Val His Gly Asp Pro Asn Val		
515 520 525		
ctg ggg ggt agg tat gag ggg agg gag gtt tgg gag agg tat agt ggg		1632
Leu Gly Gly Arg Tyr Glu Gly Arg Glu Val Trp Glu Arg Tyr Ser Gly		
530 535 540		
gag gga ggg gag gtg atg gtg ttt ggg gag ggg aat gat gaa cgt gct		1680
Glu Gly Glu Val Met Val Phe Gly Glu Gly Asn Asp Glu Arg Ala		
545 550 555 560		
ggg ggg gat gga gtt ggg gtt gcg gcg agg ttg aag agg gat gag tgg		1728
Gly Gly Asp Gly Val Gly Val Ala Ala Arg Leu Lys Arg Asp Glu Trp		
565 570 575		
ggg gtg aag gag tgt gga ttt tgg tct ggg agg agt ggg att tcc gag		1776
Gly Val Lys Glu Cys Gly Phe Trp Ser Gly Arg Ser Gly Ile Ser Glu		
580 585 590		
tga		1779

&lt;210&gt; 24

&lt;211&gt; 592

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 24

Met Leu Asn Ala Arg Ser Ile Ala Leu Ala Ser Leu Pro Val Leu Leu		
1 5 10 15		
Leu Leu Phe Ala Gln Gln Leu Ala Ser His Pro Thr Glu Gln Ile Gln		
20 25 30		
Ala Ile Leu Ala Pro Trp Val Pro Ala Ala Leu Gln Asp Val Val Leu		
35 40 45		
Tyr Asn Arg Pro Arg Val Ile Ile Pro Gln Gly Thr Val Val Gly Thr		
50 55 60		
Thr Leu Thr Asp Thr Leu Lys Ser Pro Val Asp Ala Phe Arg Gly Ile		
65 70 75 80		
Pro Tyr Ala Leu Pro Pro Ile Gly Asp Arg Arg Phe Arg Arg Ala Glu		

## 21078W0.ST25.txt

	85	90	95												
Ala	Val	His	Ala	Thr	Asp	Glu	Ile	Ile	Asp	Ala	Ser	Glu	Phe	Gly	Pro
	100			105										110	
Arg	Cys	Pro	Gly	Lys	Gln	Leu	Leu	Asn	Pro	Asn	Asp	Ile	Gly	Gly	Asp
	115			120										125	
Glu	Asp	Cys	Leu	Thr	Val	Asn	Val	Phe	Arg	Pro	His	Gly	Ala	Gln	Gly
	130			135										140	
Lys	Leu	Pro	Val	Ala	Val	Tyr	Val	His	Gly	Gly	Ala	Tyr	Asn	Arg	Gly
	145			150				155						160	
Thr	Ala	Lys	Tyr	Pro	Ala	Ser	Gly	His	Asn	Thr	Ala	Ser	Met	Val	Gly
	165				170									175	
Trp	Ser	Asp	Glu	Pro	Phe	Val	Ala	Val	Ser	Phe	Asn	Tyr	Arg	Ile	Gly
	180				185									190	
Ala	Leu	Gly	Phe	Leu	Pro	Ser	Thr	Leu	Thr	Ala	Lys	Glu	Gly	Ile	Leu
	195				200									205	
Asn	Leu	Gly	Leu	His	Asp	Gln	Ile	Leu	Leu	Gln	Trp	Val	Gln	Glu	
	210			215										220	
Asn	Ile	Ala	His	Phe	Asn	Gly	Asp	Pro	Thr	Gln	Val	Thr	Leu	Ile	Gly
	225			230				235						240	
Leu	Ser	Ala	Gly	Ala	His	Ser	Ile	Ala	His	His	Ile	Met	Asn	Tyr	Asn
	245				250									255	
Pro	Pro	Asn	Thr	Pro	Leu	Phe	His	Arg	Ala	Ile	Ile	Glu	Ser	Gly	Ala
	260				265									270	
Ala	Thr	Ser	Arg	Ala	Val	His	Pro	Tyr	Asn	Ala	Ser	Leu	His	Glu	Ser
	275				280									285	
Gln	Phe	Thr	Asp	Phe	Leu	Thr	Glu	Thr	Gly	Cys	Thr	Asn	Leu	Pro	Asp
	290				295									300	
Thr	Ala	Ile	Leu	Pro	Cys	Leu	Arg	Ala	Leu	Pro	Ser	Ser	Ala	Ile	Thr
	305			310			315							320	
Thr	Ala	Ser	Ile	Ser	Val	Phe	Asp	Lys	Tyr	Asn	Pro	Ser	Ile	Arg	Trp
	325				330									335	
Ala	Phe	Gln	Pro	Val	Ile	Asp	His	Glu	Ile	Ile	His	Arg	Arg	Pro	Ile
	340				345									350	
Asp	Ala	Trp	Arg	Ser	Gly	Lys	Trp	Asn	Arg	Met	Pro	Ile	Leu	Thr	Gly
	355				360									365	
Phe	Asn	Ser	Asn	Glu	Gly	Thr	Tyr	Tyr	Val	Pro	Arg	Asn	Leu	Ser	Leu
	370				375									380	
Ser	Glu	Asp	Phe	Thr	Ser	Phe	Phe	Arg	Thr	Leu	Leu	Pro	Ala	Tyr	Pro
	385				390			395						400	
Glu	Ser	Asp	Ile	Gln	Thr	Ile	Asp	Glu	Ile	Tyr	Pro	Asp	Pro	Asn	Val
	405				410									415	
Tyr	Ala	Thr	Ala	Ser	Pro	Tyr	Leu	Glu	Thr	Arg	Pro	Ile	Pro	Ser	Leu
	420				425									430	
Gly	Arg	Gln	Phe	Lys	Arg	Leu	Glu	Ala	Ala	Tyr	Gly	His	Tyr	Ala	Tyr

## 21078WO.ST25.txt

435	440	445
Ala Cys Pro Val Arg Gln Thr Ala Gly Phe Val Ala Asn Asp Asp Gly		
450	455	460
Cys Gly Glu Pro Val Phe Leu Tyr Arg Trp Ala Leu Asn Lys Thr Val		
465	470	475
Ile Gly Gly Ala Asn His Gly Asp Gln Met Glu Tyr Glu Thr Phe Asn		
485	490	495
Pro Ala Val Arg Asp Ile Ser Glu Ala Gln Arg Glu Val Ala Gly Leu		
500	505	510
Phe His Ala Tyr Val Thr Ser Phe Val Val His Gly Asp Pro Asn Val		
515	520	525
Leu Gly Gly Arg Tyr Glu Gly Arg Glu Val Trp Glu Arg Tyr Ser Gly		
530	535	540
Glu Gly Glu Val Met Val Phe Gly Glu Gly Asn Asp Glu Arg Ala		
545	550	555
Gly Gly Asp Gly Val Gly Val Ala Ala Arg Leu Lys Arg Asp Glu Trp		
565	570	575
Gly Val Lys Glu Cys Gly Phe Trp Ser Gly Arg Ser Gly Ile Ser Glu		
580	585	590

&lt;210&gt; 25

&lt;211&gt; 3932

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;400&gt; 25

cagataaacgt	tttgagtttgcggatcttga	ttatctcggtccaaacaga	ctgcctatc	60
cgagagatca	agtagataatgcacttagct	attagtcaaaataaacgcgg	gcagaagtct	120
attttgtcct	tttctcttttc	tttcctcgaa	gaaaaccgtggatttaactt	180
gcctcaaagt	cggctcaacc	ggcgcggtgc	caactttaaa	240
ggccgttgtg	ggggcgatgt	agatcagatc	caaattccca	300
aagaatttag	gttacatcgac	ccgataggc	tcttaatccaaacccttca	360
cttctatatg	atacatggtt	tactcctctgtttctcttcc	tccccggagg	420
gggcgcatcg	tgtctattct	tagcaaccag	cgaatttgc	480
aatcagatgt	actctacaac	ccaatcagtc	gcctaatacg	540
tcggacagcc	aacgcagaa	aagagattaa	aaaaaaa	600
aaaaggcctc	ccctcatcac	ctcaccaag	tcgcaatcaa	660
cgcgactgaa	cgtatgcatt	ccgcatggt	ttaaagtca	720
cgaaccttta	cacattcttgc	cccttccgt	agaattccaa	780
tgtttctgtg	aatgtggtgg	tttaccaccg	gctcatcgga	840
ccctgagcac	aggcaccata	gttacaacac	cagagatgt	900
cagcttcgtc	gacaatggac	tgtcatatcc	aaagaatgtc	960
tatggcatgg	cgtgtggaa	ccgatcaatt	tttgcataat	1020
tccgagaggt	ttgacatcg	ggggtttcag	tttgcataat	1080

## 21078WO.ST25.txt

tgtttcttg ccgctacttg cggcctcatt actgcccaca ctcgcttcta cacagaatgc	1140
cgatacaccc acatccgctc ctacttgtca agtccgcaat ggcacatacg agggtctcta	1200
taatcccacg tacaatcagg acttgttctt cggcataccg tatgcgcagc ctccggttgg	1260
ttagctacga ttccgtccac cacaaccgct caaacacgacg tggactggca ctcgaaatgc	1320
aacagcttat tacaatgaat gtatcggtta tggtagcgac gactggattt ggaccgacgt	1380
agtctccgaa gattgtctcg ctctcagtgt gattcgacct cacggcatcg actcaagcgc	1440
gaagctgccc gtcgtttctt gatatgcattt tgaggaaattt gcagaaggag gcactcgca	1500
ctcccggttac aacctctcctt acatcgcca acaatcccgag gagatgcaat ctcccatcat	1560
tggcgtgact gtcaactacc gccttcggg atggggattt ctctatagcc aggaagtcgc	1620
cgacgaaggc tccgccaact taggactccg cgaccaacgg cacgctctgt actggctcca	1680
agagaatatc gcttccttcg gcggcgaccc gtcgcggctc accatctggg gccaaagtgc	1740
cgggtccaaac agcgtcggtc tccatttagt ggcatacgac ggccagaatg atggcatctt	1800
ccgtgccggg atcgccgaga gcggtcccg accctccctc gcagcataca tgagcgccga	1860
agatgcacaa ccatactatg atgcccgtt caacgcaccc aactgcacccg gctttccaa	1920
cacccttact tgtctccgtt aagttccac cgacgtcctc agctccatct tcaacagctc	1980
cctcgctcgct ggggcaggat atcatccgtt cattgacggc gatttcctca gagcctcggg	2040
gatagttaat ctccagactg gccaattcgc caaaaaccccg cttcttatcg gcaccaactt	2100
cgacgaaggg accaagtatg cccctcatgg ctataatacc accgaccaat ttgtctccct	2160
cgtccaagcc aacggaacca attatacccg cgcttcacc attgcattttc tgtacccaga	2220
tgacccagcc gttggatttc cgggaaacct tcaaggtcgt cccccaccgt catacggtt	2280
ccagtgaaag cgctggctg ccttcctcgg cgatctgctc atgcacgcgc ctgcgcgcgt	2340
gacaacccag tggctggcac actggaaatgt acctgcctac gtgtatcaactt ggaacgtgat	2400
gacactaggg ccatttagatg gagccgcga tggctatgaa gtcccttca gtttccataa	2460
ttatgatggt ttggcgatg aacggggaaa cgacagcgatg acctggccac aactatcgac	2520
tatgatgtca cggatgtggg tgatctttat taatcattt gatccgattt atagtaatag	2580
tgagtgattt gccccaccta cctctggaca ctgctttagg agcttgaggg taaggaagga	2640
tgctgacacg ctgctctgct agtgacggat atccactggc ctgtctcacac aacagaaacc	2700
ccgcaaaaata tggctttga tgtcaatgtt actggactgg cttatgttga accagatacc	2760
tatagagcgg aggaaattgc gtatatcact agcattctgc agagtgcctt taatcgtag	2820
ggtagacttag aggcttcaat atcaatagat atcacacata caggagagca gcccatgttt	2880
ccctccagat caagagctat tccgtaaaaa ggtatgcattt ccccgacccg gggggaaaggc	2940
cgggggagtgc ttacctctgt gtgaaacttag aattccagca acgatggtt tagaaaggcc	3000
agatctgtt actcattgtt tgatctccg atgttgcattt cgagaaagct tctgcttgg	3060
cgtgccaagg atgttaacag ctgctgttga ggcaactcta gaaacccat agacctttac	3120
tatctcgctg actagagggt acagtaggtc ctactttgaa ttccctggcg gttggattt	3180
cgcggaaagggt tggctcaacc ctcaatgcattt gtccacgcac agcggcttggc aatgagacga	3240
gaccacgggc gattgacatg tgtcaagcag tagctatcgg gaatctgaaa aagcatggct	3300
gtcatggact ttgcaggcaa aggctgtctg ttcttagacca tcggcttagag cgccgtgagc	3360
atactaggcg agctgaaaag cctagaagcg gttgccgggtt atccgctttt tttgtgccct	3420
ttccgtttcc gggcgtaggc aatcacattt aggcaatgcc gttggggctt tggagatctc	3480
acctaaccctt attgcattttt acctcacggt gatacaacctt gatgtactat cagggaaact	3540
gagccttattt atcatcacat attagcacca cacaagctg ccaaggaaca atagtaatgt	3600
gagcgccaag gagatatctt tgaactttgtt ctccagatct tggactacat acccagccag	3660
acaggggttc gtatcgatgg ctccacagcg ggatatcatg aatcttcatg tcgtcaacgac	3720

## 21078WO.ST25.txt

tcataacctcg	agcgataggg	ccgggttatta	ctccatctgg	aaattgtcat	gactgttagag	3780
ctcagctgtc	cggatcacga	gcattatccg	tcagttata	aattccaggg	ccatcctgct	3840
caatctcaac	atgtgggctc	ttacgctgtc	atcatattag	ttagggtcca	agagaatcac	3900
agaatcattg	gcattgttct	tcatcgttcc	aa			3932

&lt;210&gt; 26

&lt;211&gt; 1518

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1518)

&lt;400&gt; 26

atg	gct	tcc	tct	gtc	ttc	ttg	ccg	cta	ctt	gct	gcc	tca	tta	ctg	ccc	48
Met	Ala	Ser	Ser	Val	Phe	Leu	Pro	Leu	Leu	Ala	Ala	Ser	Leu	Leu	Pro	
1	5	10	15													

aca	ctc	gct	tct	aca	cag	aat	gcc	gat	aca	ccg	aca	tcc	gct	cct	act	96
Thr	Leu	Ala	Ser	Thr	Gln	Asn	Ala	Asp	Thr	Pro	Thr	Ser	Ala	Pro	Thr	
20	25	30														

gtg	caa	gtc	cgc	aat	ggc	aca	tac	gag	ggt	ctc	tat	aat	ccc	acg	tac	144
Val	Gln	Val	Arg	Asn	Gly	Thr	Tyr	Glu	Gly	Leu	Tyr	Asn	Pro	Thr	Tyr	
35	40	45														

aat	cag	gac	ttg	ttc	ctc	ggc	ata	ccg	tat	gct	cag	cct	ccg	gtt	ggt	192
Asn	Gln	Asp	Leu	Phe	Leu	Gly	Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Val	Gly	
50	55	60														

gag	cta	cga	ttc	cgt	cca	caa	ccg	ctc	aac	acg	acg	tgg	act	ggc	240	
Glu	Leu	Arg	Phe	Arg	Pro	Pro	Gln	Pro	Leu	Asn	Thr	Thr	Trp	Thr	Gly	
65	70	75	80													

act	cga	aat	gca	aca	gcc	tat	tac	aat	gaa	tgt	atc	ggt	tat	ggt	agc	288
Thr	Arg	Asn	Ala	Thr	Ala	Tyr	Tyr	Asn	Glu	Cys	Ile	Gly	Tyr	Gly	Ser	
85	90	95														

gac	gac	tgg	tat	tgg	acc	gac	gta	gtc	tcc	gaa	gat	tgt	ctc	gct	ctc	336
Asp	Asp	Trp	Tyr	Trp	Thr	Asp	Val	Val	Ser	Glu	Asp	Cys	Leu	Ala	Leu	
100	105	110														

agt	gtg	att	cga	cct	cac	ggc	atc	gac	tca	agc	gct	ctg	ccc	gtc	384	
Ser	Val	Ile	Arg	Pro	His	Gly	Ile	Asp	Ser	Ser	Ala	Lys	Leu	Pro	Val	
115	120	125														

gtc	ttc	tgg	atg	cat	ggt	gga	gaa	ttc	gca	gaa	gga	ggc	act	cgc	gac	432
Val	Phe	Trp	Met	His	Gly	Gly	Glu	Phe	Ala	Glu	Gly	Gly	Thr	Arg	Asp	
130	135	140														

tcc	cgt	tac	aac	ctc	tcc	tac	atc	gtc	caa	caa	tcc	cag	gag	atg	caa	480
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 21078WO.ST25.txt

Ser Arg Tyr Asn Leu Ser Tyr Ile Val Gln Gln Ser Gln Glu Met Gln			
145	150	155	160
tct ccc atc att ggc gtg act gtc aac tac cgc ctt tcg gga tgg gga			528
Ser Pro Ile Ile Gly Val Thr Val Asn Tyr Arg Leu Ser Gly Trp Gly			
165	170	175	
ttc ctc tat agc cag gaa gtc gcc gac gaa ggc tcc gcc aac tta gga			576
Phe Leu Tyr Ser Gln Glu Val Ala Asp Glu Gly Ser Ala Asn Leu Gly			
180	185	190	
ctc cgc gac caa cgg cac gct ctg tac tgg ctc caa gag aat atc gct			624
Leu Arg Asp Gln Arg His Ala Leu Tyr Trp Leu Gln Glu Asn Ile Ala			
195	200	205	
tcc ttc ggc ggc gac ccg tcg cgg ctc acc atc tgg ggc caa agt gcc			672
Ser Phe Gly Gly Asp Pro Ser Arg Leu Thr Ile Trp Gly Gln Ser Ala			
210	215	220	
ggt gcc aac agc gtc ggt ctc cat tta gtg gca tac gac ggc cag aat			720
Gly Ala Asn Ser Val Gly Leu His Leu Val Ala Tyr Asp Gly Gln Asn			
225	230	235	240
gat ggc atc ttc cgt gcc ggg atc gcc gag agc ggc tcc gta ccc tcc			768
Asp Gly Ile Phe Arg Ala Gly Ile Ala Glu Ser Gly Ser Val Pro Ser			
245	250	255	
ctc gca gca tac atg agc gcc gaa gat gca caa cca tac tat gat gcc			816
Leu Ala Ala Tyr Met Ser Ala Glu Asp Ala Gln Pro Tyr Tyr Asp Ala			
260	265	270	
gtc gtc aac gca acc aac tgc acc ggc tct tcc aac acc ctt act tgt			864
Val Val Asn Ala Thr Asn Cys Thr Gly Ser Ser Asn Thr Leu Thr Cys			
275	280	285	
ctc cgt gaa gtt ccc acc gac gtc ctc agc tcc atc ttc aac agc tcc			912
Leu Arg Glu Val Pro Thr Asp Val Leu Ser Ser Ile Phe Asn Ser Ser			
290	295	300	
ctc gtc gct ggg gca gga tat cat ccc gtc att gac ggc gat ttc ctc			960
Leu Val Ala Gly Ala Gly Tyr His Pro Val Ile Asp Gly Asp Phe Leu			
305	310	315	320
aga gcc tcg ggg ata gtt aat ctc cag act ggc caa ttc gcc aaa acc			1008
Arg Ala Ser Gly Ile Val Asn Leu Gln Thr Gly Gln Phe Ala Lys Thr			
325	330	335	
ccg ctt ctt atc ggc acc aac ttc gac gaa ggg acc aag tat gcc cct			1056
Pro Leu Leu Ile Gly Thr Asn Phe Asp Glu Gly Thr Lys Tyr Ala Pro			
340	345	350	
cat ggc tat aat acc acc gac caa ttt gtc tcc ctc gtc caa gcc aac			1104
His Gly Tyr Asn Thr Thr Asp Gln Phe Val Ser Leu Val Gln Ala Asn			
355	360	365	
gga acc aat tat acc acc agc gct ctc acc att gca tcc ctg tac cca gat			1152
Gly Thr Asn Tyr Thr Ser Ala Leu Thr Ile Ala Ser Leu Tyr Pro Asp			
370	375	380	

## 21078WO.ST25.txt

gac cca gcc gtt ggt att ccg gga acc ctt caa ggt cgt ccc cca ccc Asp Pro Ala Val Gly Ile Pro Gly Thr Leu Gln Gly Arg Pro Pro Pro 385 390 395 400	1200
tca tac ggt tac cag tgg aag cgc gtg gct gcc ttc ctc ggc gat ctg Ser Tyr Gly Tyr Gln Trp Lys Arg Val Ala Ala Phe Leu Gly Asp Leu 405 410 415	1248
ctc atg cac gcg cct cgc cgc gtg aca acc cag tgg ctg gca cac tgg Leu Met His Ala Pro Arg Arg Val Thr Thr Gln Trp Leu Ala His Trp 420 425 430	1296
aat gta cct gcc tac gtg tat cac tgg aac gtg atg aca cta ggg cca Asn Val Pro Ala Tyr Val Tyr His Trp Asn Val Met Thr Leu Gly Pro 435 440 445	1344
tta gat gga gcc gcg cat ggc tat gaa gtc ccc ttc agt ttc cat aat Leu Asp Gly Ala Ala His Gly Tyr Glu Val Pro Phe Ser Phe His Asn 450 455 460	1392
tat gat ggt ttg ggc gat gaa cgg gga aac gac agc gtg acc tgg cca Tyr Asp Gly Leu Gly Asp Glu Arg Gly Asn Asp Ser Val Thr Trp Pro 465 470 475 480	1440
caa cta tcg act atg atg tca cgg atg tgg gtg agc ttt att aat cat Gln Leu Ser Thr Met Met Ser Arg Met Trp Val Ser Phe Ile Asn His 485 490 495	1488
ttg gat ccg aat tat agt aat agt gag tga Leu Asp Pro Asn Tyr Ser Asn Ser Glu 500 505	1518

&lt;210&gt; 27

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 27

Met Ala Ser Ser Val Phe Leu Pro Leu Leu Ala Ala Ser Leu Leu Pro 1 5 10 15	
Thr Leu Ala Ser Thr Gln Asn Ala Asp Thr Pro Thr Ser Ala Pro Thr 20 25 30	
Val Gln Val Arg Asn Gly Thr Tyr Glu Gly Leu Tyr Asn Pro Thr Tyr 35 40 45	
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly 50 55 60	
Glu Leu Arg Phe Arg Pro Pro Gln Pro Leu Asn Thr Thr Trp Thr Gly 65 70 75 80	
Thr Arg Asn Ala Thr Ala Tyr Tyr Asn Glu Cys Ile Gly Tyr Gly Ser 85 90 95	

## 21078WO.ST25.txt

Asp Asp Trp Tyr Trp Thr Asp Val Val Ser Glu Asp Cys Leu Ala Leu  
                  100                 105                 110  
 Ser Val Ile Arg Pro His Gly Ile Asp Ser Ser Ala Lys Leu Pro Val  
                  115                 120                 125  
 Val Phe Trp Met His Gly Gly Glu Phe Ala Glu Gly Thr Arg Asp  
                  130                 135                 140  
 Ser Arg Tyr Asn Leu Ser Tyr Ile Val Gln Gln Ser Gln Glu Met Gln  
                  145                 150                 155                 160  
 Ser Pro Ile Ile Gly Val Thr Val Asn Tyr Arg Leu Ser Gly Trp Gly  
                  165                 170                 175  
 Phe Leu Tyr Ser Gln Glu Val Ala Asp Glu Gly Ser Ala Asn Leu Gly  
                  180                 185                 190  
 Leu Arg Asp Gln Arg His Ala Leu Tyr Trp Leu Gln Glu Asn Ile Ala  
                  195                 200                 205  
 Ser Phe Gly Gly Asp Pro Ser Arg Leu Thr Ile Trp Gly Gln Ser Ala  
                  210                 215                 220  
 Gly Ala Asn Ser Val Gly Leu His Leu Val Ala Tyr Asp Gly Gln Asn  
                  225                 230                 235                 240  
 Asp Gly Ile Phe Arg Ala Gly Ile Ala Glu Ser Gly Ser Val Pro Ser  
                  245                 250                 255  
 Leu Ala Ala Tyr Met Ser Ala Glu Asp Ala Gln Pro Tyr Tyr Asp Ala  
                  260                 265                 270  
 Val Val Asn Ala Thr Asn Cys Thr Gly Ser Ser Asn Thr Leu Thr Cys  
                  275                 280                 285  
 Leu Arg Glu Val Pro Thr Asp Val Leu Ser Ser Ile Phe Asn Ser Ser  
                  290                 295                 300  
 Leu Val Ala Gly Ala Gly Tyr His Pro Val Ile Asp Gly Asp Phe Leu  
                  305                 310                 315                 320  
 Arg Ala Ser Gly Ile Val Asn Leu Gln Thr Gly Gln Phe Ala Lys Thr  
                  325                 330                 335  
 Pro Leu Leu Ile Gly Thr Asn Phe Asp Glu Gly Thr Lys Tyr Ala Pro  
                  340                 345                 350  
 His Gly Tyr Asn Thr Thr Asp Gln Phe Val Ser Leu Val Gln Ala Asn  
                  355                 360                 365  
 Gly Thr Asn Tyr Thr Ser Ala Leu Thr Ile Ala Ser Leu Tyr Pro Asp  
                  370                 375                 380  
 Asp Pro Ala Val Gly Ile Pro Gly Thr Leu Gln Gly Arg Pro Pro Pro  
                  385                 390                 395                 400  
 Ser Tyr Gly Tyr Gln Trp Lys Arg Val Ala Ala Phe Leu Gly Asp Leu  
                  405                 410                 415  
 Leu Met His Ala Pro Arg Arg Val Thr Thr Gln Trp Leu Ala His Trp  
                  420                 425                 430  
 Asn Val Pro Ala Tyr Val Tyr His Trp Asn Val Met Thr Leu Gly Pro  
                  435                 440                 445

## 21078WO.ST25.txt

Leu Asp Gly Ala Ala His Gly Tyr Glu Val Pro Phe Ser Phe His Asn  
 450 455 460  
 Tyr Asp Gly Leu Gly Asp Glu Arg Gly Asn Asp Ser Val Thr Trp Pro  
 465 470 475 480  
 Gln Leu Ser Thr Met Met Ser Arg Met Trp Val Ser Phe Ile Asn His  
 485 490 495  
 Leu Asp Pro Asn Tyr Ser Asn Ser Glu  
 500 505

&lt;210&gt; 28

&lt;211&gt; 3091

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;400&gt; 28

ggcgaacggg cctgagcgtg	cgtcggaggc	agaagttagag	ccgggactat	ggatattggc	60
gaggaatata ttatagtaga	ttatagggag	tcaatgcag	ctcggattgg	tttggttactt	120
ttagtcagat ggacattgtt	ggaaaagatg	aacgcgacgg	aaaaaaaaca	tgaggatttg	180
cggggatttc gtcacatgca	gaggcgcgga	ttttcccctc	cgattttact	tcctcaactc	240
tcctttctct ttcatttcca	tccgatttga	gtccaaactca	tctcactcga	agaatctcat	300
taatttcagg gtcctgctca	gcccagtcaa	gtttccttag	tttcgatctt	tcagttggcc	360
cgtcatgtcc attgaccagg	aatggagcaa	gccccgatga	ggatcggcca	gcggagacaa	420
ctgccaatcc ttggtatcca	tacccttaac	agcgcaatgg	caccagctct	ctgcccattc	480
acgtcatctg cacagcctag	ctgcccatta	gccttgaccc	cttctactt	gcggcatcag	540
tgccgctgat actagcccc	acagagtgtt	tctcccttcg	actgtggctc	ggaacgtggg	600
ggcgggttcc aagttcttat	gccccaggtt	gttggctag	ccttgctcat	ctgggtggcc	660
agcacaccc ccatacaata	ggatccgtgg	tgttggcagg	attcttgtca	tttcgcctatg	720
tcgaatcacc gcatgcggaa	ggaggacgcc	ttgccttgca	atgtttctc	cacatctgcg	780
accctattgt tcagaccctg	gagccgattc	cgcgagatgt	attcctgccc	ggccactgaa	840
agtgccttat aacgtctggg	gtgtcctttt	attgtatgaga	gcatgatctt	tcgcgttaca	900
gttctcacaa tcggtaaag	cattcgtggc	cccgaggctc	gttgacaaac	acaatatgat	960
tttctttcat ctggcaccgt	tcttcatttct	ctttggctta	gtatgtatctt	ctcagaaccc	1020
tacgggtggac ctggctaca	caagatataa	aggcaaattct	ctgccccatg	gtatcagtca	1080
gtggctgggg atacgctacg	cggctgcacc	taccgggtct	ctgcgggtct	ctgcgccaca	1140
ggatcctgac acggtagatg	gcgttcaaga	agcattcaag	gtatggttt	ttctacaata	1200
aataaaaaga tatattgcga	gtctgtgctt	tgctaataacc	cagggcacag	catggcccc	1260
ggtgtgttcc caccagccaa	tatcccaactc	ccgcaggcac	gtccgaggat	tgtctttcc	1320
tcgatgtata cgctcccagc	tcgggtggaaag	ctactacgag	gctgcccgtt	ttcggttgaa	1380
ttcaaggagg cggcttcaat	gccaaactcca	gcccccaacta	caatggaaaca	ggattgatcg	1440
aagcggccaa tatgtccatg	gtgggtgtca	ccttcaacta	cagggtcggt	ccgtacgggt	1500
tcctctctgg atccgaggtg	ctggaggggag	gaagcgtgaa	caatggcctg	aaggaccaaa	1560
tcaaggcct gaagtgggtg	caagagcata	tcagcaaggt	atgcggacac	tcaccaaccc	1620
acagcaaatac accgctaatt	gcagccgcag	tttggaggcg	atcccagtca	cggtgttata	1680

## 21078WO.ST25.txt

ggcggcgaca	gcmcaggcgc	agcgctatc	actctccatc	tttcagccca	cggtggcaga	1740
gacgacgaac	tattccacgc	tgccgccgca	gagtcccaa	gctttgtcc	tatgttacc	1800
gtcaatcaa	gccaattcgc	ctataacaac	ctggcatcc	gcccggctg	cgcaagcgat	1860
tcagacaccc	tcgcctgctt	acgcccacta	aacaccacag	aactgcagcg	catcaacatc	1920
aacacaccct	tacccaccgc	ccaacaagca	cctcttacc	tgtacggtcc	cgtcgac	1980
ggctccctca	tcccagacta	cacataccgg	cttttccagc	aaggcaaatt	catcaaagtc	2040
cccgtaatct	tcggcgacga	caccaacgaa	ggaacaatct	tcgtccccaa	aacgacctcc	2100
accgtcgccg	aagccgacac	cttcatccaa	gaccaattcc	ccaacatcaa	cttcacccac	2160
ctaaccaagc	tgaacgactg	gtatctcaa	aaaaaccaa	ctcgcgagtt	ccccaaattcc	2220
tccccctact	ggcgtcccgc	tagcaccgcg	tacggtaaaa	tcagatatat	ctgtccgggg	2280
atctacatgt	cctctgtgtt	tgcttagtgcc	ggtgtcaaca	gctggaacta	tcattatgct	2340
gtgcaggacc	ccgcccggaa	agcctcaggc	agaggtgtca	gtcatactgt	ggaagaaaaat	2400
gccattttgg	gcccgcagta	tgtgagtggc	acaccgcgg	cgtcgatct	cactgagaat	2460
gcccatttgc	tgccgggtat	gcagggctac	tggacgagtt	tcattagagt	gtttgatccg	2520
aatccgctga	ggtatccggg	gagtccggag	tggaaagacgt	ggagtgtatgg	acatggggag	2580
gattatcggc	ggtatattgt	ccgcacgaat	gagacgagga	tggagacggt	gtcggaggcg	2640
cagaggaaaa	ggtgcgaata	ttggagtagt	gttggccgg	acttgtcgca	gtgattgcac	2700
tttattatctt	tgttcggtgg	taaggtatat	atatacatat	tataatattg	taagctatag	2760
agtgtatggta	cgtgaattga	atataatggag	aaagatggtc	ttgtataaaat	caaaacattc	2820
ttttttggct	gccattccac	gatcatcatt	ccaatgatc	aaaccaagta	actataaccg	2880
aatatataca	tcttatataa	cctgcttctc	atcagaatta	ccaaaagacg	ggtccggcac	2940
acacagctag	accgagcaga	tacgtcgaca	tgaacccagg	tgtgaaaca	taatgcaaca	3000
aaagaaaagag	aaaagaaggc	aaaacaagtg	agaagcacta	ctgctccaca	tagagcagta	3060
aacgaacgat	gaatgaggga	tatcatcatc	a			3091

<210> 29  
<211> 1617  
<212> DNA  
<213> *Aspergillus niger*

<220>  
<221> CDS  
<222> (1)..(1617)

<400> 29						
atg att ttc ttt cat ctg gca ccg ttc ttc ttt ctc ttt ggt cta gta						48
Met Ile Phe Phe His Leu Ala Pro Phe Phe Phe Leu Phe Gly Leu Val						
1	5	10	15			
gta tct tct cag aac cct acg gtg gac ctt ggc tac aca aga tat aaa						96
Val Ser Ser Gln Asn Pro Thr Val Asp Leu Gly Tyr Thr Arg Tyr Lys						
20	25	30				
ggc aaa tct ctg ccc aat ggt atc agt cag tgg ctg ggg ata cgc tac						144
Gly Lys Ser Leu Pro Asn Gly Ile Ser Gln Trp Leu Gly Ile Arg Tyr						

## 21078WO.ST25.txt

35	40	45	
gcg gct gca cct acc ggg tct ctg cggttc tct gcgcacat ccc Ala Ala Ala Pro Thr Gly Ser Leu Arg Phe Ser Ala Pro Gln Asp Pro			192
50	55	60	
gac acg gta gat ggc gtt caa gaa gca ttcaag cat ggt ccc cgg tgt Asp Thr Val Asp Gly Val Gln Glu Ala Phe Lys His Gly Pro Arg Cys			240
65	70	75	80
gtt ccc acc agc caa tat ccc act ccc gca ggc acg tcc gag gat tgt Val Pro Thr Ser Gln Tyr Pro Thr Pro Ala Gly Thr Ser Glu Asp Cys			288
85	90	95	
ctc ttc ctc gat gta tac gct ccc agc tcg gtg gaa gct act acg agg Leu Phe Leu Asp Val Tyr Ala Pro Ser Ser Val Glu Ala Thr Thr Arg			336
100	105	110	
ctg ccc gtt ttc gtt tgg att caa gga ggc ggc ttc aat gcc aac tcc Leu Pro Val Phe Val Trp Ile Gln Gly Gly Phe Asn Ala Asn Ser			384
115	120	125	
agc ccc aac tac aat gga aca gga ttg atc gaa gcgc aat atg tcc Ser Pro Asn Tyr Asn Gly Thr Gly Leu Ile Glu Ala Ala Asn Met Ser			432
130	135	140	
atg gtg gtc acc ttc aac tac agg gtc ggt ccgtac ggg ttc ctc Met Val Val Thr Phe Asn Tyr Arg Val Gly Pro Tyr Gly Phe Leu			480
145	150	155	160
tct gga tcc gag gtg ctg gag gga agc gtg aac aat ggc ctg aag Ser Gly Ser Glu Val Leu Glu Gly Gly Ser Val Asn Asn Gly Leu Lys			528
165	170	175	
gac caa atc aag gtc ctg aag tgg gtg caa gag cat atc agc aag ttt Asp Gln Ile Lys Val Leu Lys Trp Val Gln Glu His Ile Ser Lys Phe			576
180	185	190	
gga ggc gat ccc agt cac gtt gtt atc ggc ggc gac agc gca ggc gca Gly Gly Asp Pro Ser His Val Val Ile Gly Gly Asp Ser Ala Gly Ala			624
195	200	205	
gcg tct atc act ctc cat ctt tca gcc cac ggt ggc aga gac gac gaa Ala Ser Ile Thr Leu His Leu Ser Ala His Gly Gly Arg Asp Asp Glu			672
210	215	220	
cta ttc cac gct gcc gca gag tcc caa agc ttt gct cct atg ttg Leu Phe His Ala Ala Ala Glu Ser Gln Ser Phe Ala Pro Met Leu			720
225	230	235	240
acc gtc aat caa agc caa ttc gcc tat aac aac ctg gtc atc cgc gcc Thr Val Asn Gln Ser Gln Phe Ala Tyr Asn Asn Leu Val Ile Arg Ala			768
245	250	255	
ggc tgc gca agc gat tca gac acc ctc gcc tgc tta cgc cga cta aac. Gly Cys Ala Ser Asp Ser Asp Thr Leu Ala Cys Leu Arg Arg Leu Asn			816
260	265	270	
acc aca gaa ctg cag cgc atc aac atc aac aca ccc tta ccc acc gcc			864

## 21078WO.ST25.txt

Thr Thr Glu Leu Gln Arg Ile Asn Ile Asn Thr Pro Leu Pro Thr Ala			
275	280	285	
caa caa gca cct ctc tac ctg tac ggt ccc gtc gtc gac ggc tcc ctc			912
Gln Gln Ala Pro Leu Tyr Leu Tyr Gly Pro Val Val Asp Gly Ser Leu			
290	295	300	
atc cca gac tac aca tac cgg ctt ttc cag caa ggc aaa ttc atc aaa			960
Ile Pro Asp Tyr Thr Tyr Arg Leu Phe Gln Gln Gly Lys Phe Ile Lys			
305	310	315	320
gtc ccc gta atc ttc ggc gac gac acc aac gaa gga aca atc ttc gtc			1008
Val Pro Val Ile Phe Gly Asp Asp Thr Asn Glu Gly Thr Ile Phe Val			
325	330	335	
ccc aaa acg acc tcc acc gtc ggc gaa gcc gac acc ttc atc caa gac			1056
Pro Lys Thr Thr Ser Thr Val Gly Glu Ala Asp Thr Phe Ile Gln Asp			
340	345	350	
caa ttc ccc aac atc aac ttc acc cac cta acc aag ctg aac gac tgg			1104
Gln Phe Pro Asn Ile Asn Phe Thr His Leu Thr Lys Leu Asn Asp Trp			
355	360	365	
tat ctc aaa gaa aac caa act cgc gag ttc ccc aat tcc tcc ccc tac			1152
Tyr Leu Lys Glu Asn Gln Thr Arg Glu Phe Pro Asn Ser Ser Pro Tyr			
370	375	380	
tgg cgt ccc gct agc acc gcg tac ggt gaa atc aga tat atc tgt ccg			1200
Trp Arg Pro Ala Ser Thr Ala Tyr Gly Glu Ile Arg Tyr Ile Cys Pro			
385	390	395	400
ggg atc tac atg tcc tct gtg ttt gct agt gcc ggt gtc aac agc tgg			1248
Gly Ile Tyr Met Ser Ser Val Phe Ala Ser Ala Gly Val Asn Ser Trp			
405	410	415	
aac tat cat tat gct gtg cag gac ccc gcc gcg gaa gcc tca ggc aga			1296
Asn Tyr His Tyr Ala Val Gln Asp Pro Ala Ala Glu Ala Ser Gly Arg			
420	425	430	
ggt gtc agt cat act gtg gaa gaa aat gcc att tgg ggc ccg cag tat			1344
Gly Val Ser His Thr Val Glu Glu Asn Ala Ile Trp Gly Pro Gln Tyr			
435	440	445	
gtg agt ggc aca ccg ccg gcg tcg tat ctc act gag aat gcg cca att			1392
Val Ser Gly Thr Pro Pro Ala Ser Tyr Leu Thr Glu Asn Ala Pro Ile			
450	455	460	
gtg ccg gtg atg cag ggc tac tgg acg agt ttc att aga gtg ttt gat			1440
Val Pro Val Met Gln Gly Tyr Trp Thr Ser Phe Ile Arg Val Phe Asp			
465	470	475	480
ccg aat ccg ctg agg tat ccg ggg agt ccg gag tgg aag acg tgg agt			1488
Pro Asn Pro Leu Arg Tyr Pro Gly Ser Pro Glu Trp Lys Thr Trp Ser			
485	490	495	
gat gga cat ggg gag gat tat ccg ccg ata ttt gtc cgc acg aat gag			1536
Asp Gly His Gly Glu Asp Tyr Arg Arg Ile Phe Val Arg Thr Asn Glu			
500	505	510	

21078W0.ST25.txt

acg agg atg gag acg gtg tcg gag gcg cag agg gaa agg tgc gaa tat 1584  
 Thr Arg Met Glu Thr Val Ser Glu Ala Gln Arg Glu Arg Cys Glu Tyr  
                   515              520              525  
 tgg agt agt gtt ggg ccg gac ttg tcg cag tga 1617  
 Trp Ser Ser Val Gly Pro Asp Leu Ser Gln  
                   530              535

<210> 30  
<211> 538  
<212> PRT  
<213> *Aspergillus niger*

<400> 30  
 Met Ile Phe Phe His Leu Ala Pro Phe Phe Leu Phe Gly Leu Val  
 1 5 10 15  
 Val Ser Ser Gln Asn Pro Thr Val Asp Leu Gly Tyr Thr Arg Tyr Lys  
 20 25 30  
 Gly Lys Ser Leu Pro Asn Gly Ile Ser Gln Trp Leu Gly Ile Arg Tyr  
 35 40 45  
 Ala Ala Ala Pro Thr Gly Ser Leu Arg Phe Ser Ala Pro Gln Asp Pro  
 50 55 60  
 Asp Thr Val Asp Gly Val Gln Glu Ala Phe Lys His Gly Pro Arg Cys  
 65 70 75 80  
 Val Pro Thr Ser Gln Tyr Pro Thr Pro Ala Gly Thr Ser Glu Asp Cys  
 85 90 95  
 Leu Phe Leu Asp Val Tyr Ala Pro Ser Ser Val Glu Ala Thr Thr Arg  
 100 105 110  
 Leu Pro Val Phe Val Trp Ile Gln Gly Gly Phe Asn Ala Asn Ser  
 115 120 125  
 Ser Pro Asn Tyr Asn Gly Thr Gly Leu Ile Glu Ala Ala Asn Met Ser  
 130 135 140  
 Met Val Val Val Thr Phe Asn Tyr Arg Val Gln Pro Tyr Gly Phe Leu  
 145 150 155 160  
 Ser Gly Ser Glu Val Leu Glu Gly Gly Ser Val Asn Asn Gly Leu Lys  
 165 170 175  
 Asp Gln Ile Lys Val Leu Lys Trp Val Gln Glu His Ile Ser Lys Phe  
 180 185 190  
 Gly Gly Asp Pro Ser His Val Val Ile Gly Gly Asp Ser Ala Gly Ala  
 195 200 205  
 Ala Ser Ile Thr Leu His Leu Ser Ala His Gly Gly Arg Asp Asp Glu  
 210 215 220  
 Leu Phe His Ala Ala Ala Glu Ser Gln Ser Phe Ala Pro Met Leu  
 225 230 235 240

## 21078WO.ST25.txt

Thr Val Asn Gln Ser Gln Phe Ala Tyr Asn Asn Leu Val Ile Arg Ala  
                  245                 250                 255  
 Gly Cys Ala Ser Asp Ser Asp Thr Leu Ala Cys Leu Arg Arg Leu Asn  
                  260                 265                 270  
 Thr Thr Glu Leu Gln Arg Ile Asn Ile Asn Thr Pro Leu Pro Thr Ala  
                  275                 280                 285  
 Gln Gln Ala Pro Leu Tyr Leu Tyr Gly Pro Val Val Asp Gly Ser Leu  
                  290                 295                 300  
 Ile Pro Asp Tyr Thr Tyr Arg Leu Phe Gln Gln Gly Lys Phe Ile Lys  
                  305                 310                 315                 320  
 Val Pro Val Ile Phe Gly Asp Asp Thr Asn Glu Gly Thr Ile Phe Val  
                  325                 330                 335  
 Pro Lys Thr Thr Ser Thr Val Gly Glu Ala Asp Thr Phe Ile Gln Asp  
                  340                 345                 350  
 Gln Phe Pro Asn Ile Asn Phe Thr His Leu Thr Lys Leu Asn Asp Trp  
                  355                 360                 365  
 Tyr Leu Lys Glu Asn Gln Thr Arg Glu Phe Pro Asn Ser Ser Pro Tyr  
                  370                 375                 380  
 Trp Arg Pro Ala Ser Thr Ala Tyr Gly Glu Ile Arg Tyr Ile Cys Pro  
                  385                 390                 395                 400  
 Gly Ile Tyr Met Ser Ser Val Phe Ala Ser Ala Gly Val Asn Ser Trp  
                  405                 410                 415  
 Asn Tyr His Tyr Ala Val Gln Asp Pro Ala Ala Glu Ala Ser Gly Arg  
                  420                 425                 430  
 Gly Val Ser His Thr Val Glu Glu Asn Ala Ile Trp Gly Pro Gln Tyr  
                  435                 440                 445  
 Val Ser Gly Thr Pro Pro Ala Ser Tyr Leu Thr Glu Asn Ala Pro Ile  
                  450                 455                 460  
 Val Pro Val Met Gln Gly Tyr Trp Thr Ser Phe Ile Arg Val Phe Asp  
                  465                 470                 475                 480  
 Pro Asn Pro Leu Arg Tyr Pro Gly Ser Pro Glu Trp Lys Thr Trp Ser  
                  485                 490                 495  
 Asp Gly His Gly Glu Asp Tyr Arg Arg Ile Phe Val Arg Thr Asn Glu  
                  500                 505                 510  
 Thr Arg Met Glu Thr Val Ser Glu Ala Gln Arg Glu Arg Cys Glu Tyr  
                  515                 520                 525  
 Trp Ser Ser Val Gln Pro Asp Leu Ser Gln  
                  530                 535

&lt;210&gt; 31

&lt;211&gt; 4575

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

## 21078WO.ST25.txt

&lt;400&gt; 31

gatcaactt cagtcaaatt gagacgattt taactcatca tcgcacatctca catggaaagg	60
ttgtacaccc aacaattaga cctcaacata tttcacggat attcctgcaa gatatataat	120
aaagccatca ctccactttg gtagatatgt tagccaaccg ggtttgagcg agtttcttga	180
atggactcat taagggtagg atcaattctg atgtccacaa ttggcccta tttgccagat	240
gtaggcccag agaattcggt atcttcaga tttgcgtgc tatcccggtt tccagtaaac	300
tattaggttc ggctcggtca caccagacag acacgactga cccatgcgtc gccaggaatc	360
ctgataggcc tagcagtccc gcgtgcacat atcggcttgg tagaaaagga tagccgtgaa	420
tgtataatct ttcatatgtac ggttaaatgc gtttctgtat ggtgagaagc tgtgttagatg	480
ggagatgagc tgtaaatggc ttgcagtgg caacctctag gctgctgcag gccggaatac	540
tgcatggcgt gattttcgtc gtgaatcttgc ttcatatataca ggtgtaaaac acacgtaagg	600
aaaatcttgt tatagcaggg ttgaaaacag ttgctagaat tggcagtgcac tggcgtgtt	660
gcaagggttt atttgcacc ttgaagtac actgcgttgc gtcaaaggca aatcacccca	720
tcaagtaata aatatataatc tctgttatca agtcggctcc tctagtagtg cagcctcagt	780
acagacaaca gggactaaca gcactttgc tggtgagctt gagcgcaccc caccttctc	840
tccggcctct ttctgtatttgc gcatttcaat ggcctgttat gggacttctg agcctgttgc	900
attgagtgat atggtagtgatc gagcgcaaaa aaggtgattt tcaaacacca tggatgcaag	960
tcagaggtaa gtgcgagagg gagatcagga ggaggagagc tttatataag gccgcgtagg	1020
cggcagagac gcaagagacat ctggtaagt accagcattc agtgaatttt ataacagttat	1080
tatttgcattt cacgactctg cattgccttt aataagctcg gcgtatattt gtagggaccc	1140
taggttgaa tagccccagg ggggcttggt gtcgggttgatc gagcttgcgtc cccgagattc	1200
attttacacc tagtcaggaa tccggcggg ttttatacct ccctggaggc ggaatgtacc	1260
tttgcatttca ctgaaaattt cggccattttt gttctatttt actggctatg gggtttgcacca	1320
ctatcgctca catcctcgca aggacaccc cgatactgca gtcaaacgtg ggagttgccg	1380
atagaaacta caagatcaaa tctcgatccc tgggttggac ggtcacattc ggtgaaagag	1440
gtttatcttc gctccaacca gccttcatttgc tcgggcgtc agtgcataag atccaagcaa	1500
ttttaaacac tttactccac tagtcacact gttttagcag tgcattgcctc tgaatcagga	1560
ctaaactccg attttctca gtgaatactg ctaaagacaa ttatgatcct acagactatc	1620
tctgtaaaaa agcgcagttt acttctcgatc aatcatgaag ccatttttagtgc ctttctccg	1680
tcaatcattt acccctacttgc ttgactatattt cagccctaag ggaataaaaac atttgcgtt	1740
gaggtgaact ataactcaat caatgactga aagcttaacg tatctcacaa ttcatctcac	1800
cgtgaagagt catttacatt tacgatccag ccaggccgcg ctgacatcag caggcgtgag	1860
agcgcatttca tgcttgcgtc gacataagcc gaatccatttgcatgatgcgtc cttcccgaa	1920
agagttatggg tttccgttactt gaccatgtca gtggcccat atggctctca actacacgaa	1980
cacagacattt tatcgttccca ggtccccaca actttaatcc ggagatgcgg ggggtgcagga	2040
atggaaacacg gatacatgtg tggatgttag gaccaaacaa attggctgtc gtggacattc	2100
gactcgactt gacccttcaat tgcgttggcc ggaggactga gccatagggttataagaacac	2160
cgtgtactt catgcctcgatc tatcgatccc ctatcatttgcatgatc caggaagaca	2220
tagcatgacc gtgaacacga tgaaggaaat gctccgcacg cttagttggatc tggcacttgg	2280
catggccacgc ctggcaacctt gacccaaccc agtagccacg acaaaagaacg gaagtttata	2340
tgggtcttac atgcctcagt ataatgagga ttatccat ggaattccat ttgctaaagcc	2400
cccggttggca cacttgcgtt gggccaaaccc cgagacttgcattt aatgagtttgcgtt ggtcgggatt	2460
gcgcctgtc acccgctatgc cgtatggtaag tagcctgaac agactgctaa acgaccatgt	2520

## 21078WO.ST25.txt

acttactaac	agcgcgtgt	ataggaatgt	ataggtaacg	gcagtgatca	aaaaggattat	2580
ctgcaggtga	ggatttgacg	ccacttctt	tacgctgttc	tctactaacc	agcaaaatag	2640
agcgaggact	gtctctacct	aaacgtggtc	cgtcccgctg	aatacgacaa	tgccagtc	2700
ccagtcctt	tgatggattca	tggtatgtag	tgaaatctac	ctcaacgaca	agttactccc	2760
gacgctgaat	gaacaaaaca	ggcggtggct	tcgcacaagg	cggcactccc	gaccttcgat	2820
acaatcttac	atttattgtt	gaacactcgg	tcaatatcgg	ccagccaatt	atgcagtc	2880
gcgttgccta	tcgtctcggt	ccttggggtt	tcttcaatgg	ggtcagtc	gccaatgagg	2940
gatcgtaaa	tctcgggctg	aaggaccagc	gcttggccct	gcattgggtg	aaagagaaca	3000
ttgcagggtt	cgggtgggg	tttccataaa	gctattaaac	gtacacagtc	caaaattact	3060
aatgacagtc	actcctatac	aggcgaccct	agtaaagtgc	tgatttacgg	acaaagtgc	3120
ggctccgaaa	gctggggata	ccaaatccgc	gcgtacaacg	gccgagatga	cgggctcttc	3180
cgcggaggca	tgatggagtc	cggcgcgg	ttacctggca	gtgccttcaa	cctcacctgg	3240
acatatgagc	cttgggttcca	gcaaatacg	gacgaggcag	gatgttccc	gaccaccgc	3300
aaactggact	gtctacgccc	cacgccttc	acagtcctaa	acaacattct	gaacaccacc	3360
gccaacgaca	cgacgcctta	caactggagg	cccacagtgg	acggtgactt	cgtagcgc	3420
tatcccagcg	agcaactcg	cacaggagac	ttcgtcaaa	taccaatcat	aatcggtac	3480
accacggacg	aaggaacaac	agagtgc	gaaccagtga	acaccaccgc	cgaattaaaa	3540
gaataacctca	gctgtacgta	cctccttccc	ttcctccctt	atccccccat	ccccatccca	3600
ataacaccaa	cccaagcaaca	acaacctacg	gctggccct	cgactcacag	gtatgtatcc	3660
cgctccttga	cctctacccc	aacaccacct	ccttcggcat	cccatcatcc	gaagaactcg	3720
gcggcaacgt	cacccccc	cagccctacg	gcccgcatt	ccgcccagacg	gcagcatact	3780
acggcgacgc	ccagttcata	gccgcgacgc	gctacacctg	tgagctatgg	gcggcacata	3840
acctgacagc	atattgctac	cgattcaaca	ccaagacaga	cgattacaac	aggaaagaag	3900
gcgtggcgca	tttctcgac	gtgatttca	tcttcaacaa	ccttaatgg	tatgggttca	3960
gtccgaaccc	gttcaccaat	gctccagaga	gtataactga	gcttagctac	ctcatgtccg	4020
gctcggtat	cagttcact	aatagtctgg	atcctaataa	gtggactggt	cgcggaaagga	4080
acgctacgaa	gacggagaat	tggccgtgt	atgatctgg	gaatccctt	agtatgtatct	4140
gggatgcgaa	tgtcacttcg	tatgcggcgc	cggatacttg	gcgtaaggag	ggtattgcgt	4200
tgattaatgc	taatcgagg	gcgtatcaga	ggtgaatgt	gtgtagctt	cagccgttgc	4260
ctacttgtt	gactttcaaa	ctcaaaaactt	tctattgaga	gagaaaattt	tgcgaggaaa	4320
gtactaccgc	gggcagaaca	ctctgcgcac	aggccatat	ctacaaaactc	actgaacaga	4380
gtctatagca	gatttaggt	attgtcaagc	ttacatacag	acataacccc	accacaat	4440
cgtggtaaga	tagcacattt	ctttaaagaa	aaaaaaa	gatgaataca	tataatcg	4500
tacgtcaata	attcaaaaaca	gaatatgtca	gctgtgcaca	catccgacca	ttacactagt	4560
aaagtgagcg	gcggc					4575

&lt;210&gt; 32

&lt;211&gt; 1695

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; CDS

## 21078WO.ST25.txt

&lt;222&gt; (1)..(1695)

&lt;400&gt; 32

atg aag gga atg ctc ccg acg ctt agt tgg ttg gca ctg ggc atg gcc	48
Met Lys Gly Met Leu Pro Thr Leu Ser Trp Leu Ala Leu Gly Met Ala	
1               5               10               15	
agc ctg gca acc tgc acc aac cca gta gcc cag aca aag aac gga agt	96
Ser Leu Ala Thr Cys Thr Asn Pro Val Ala Gln Thr Lys Asn Gly Ser	
20               25               30	
tat tat ggt gtc tac atg cct cag tat aat gag gat tat ttt ctt gga	144
Tyr Tyr Gly Val Tyr Met Pro Gln Tyr Asn Glu Asp Tyr Phe Leu Gly	
35               40               45	
att cca ttt gct aag ccc ccg ttg gca cac ttg cgt tgg gcc aac ccc	192
Ile Pro Phe Ala Lys Pro Pro Leu Ala His Leu Arg Trp Ala Asn Pro	
50               55               60	
gag agt ctt aat gag tct tgg tcg gga ttg cgc cct gct acc ggc tat	240
Glu Ser Leu Asn Glu Ser Trp Ser Gly Leu Arg Pro Ala Thr Gly Tyr	
65               70               75               80	
gcg atg gaa tgt ata ggt tac ggc agt gat caa aaa ggt tat ctg cag	288
Ala Met Glu Cys Ile Gly Tyr Ser Asp Gln Lys Gly Tyr Leu Gln	
85               90               95	
agc gag gac tgt ctc tac cta aac gtg gtc cgt ccc gct gaa tac gac	336
Ser Glu Asp Cys Leu Tyr Leu Asn Val Val Arg Pro Ala Glu Tyr Asp	
100               105               110	
aat gcc agt ctt cca gtc ctt gta tgg att cat ggc ggt ggc ttc gca	384
Asn Ala Ser Leu Pro Val Leu Val Trp Ile His Gly Gly Phe Ala	
115               120               125	
caa ggc ggc act ccc gac ctt cga tac aat ctt aca ttt att gtt gaa	432
Gln Gly Gly Thr Pro Asp Leu Arg Tyr Asn Leu Thr Phe Ile Val Glu	
130               135               140	
cac tcg gtc aat atc ggc cag cca att atc gca gtg agc gtt gcc tat	480
His Ser Val Asn Ile Gly Gln Pro Ile Ile Ala Val Ser Val Ala Tyr	
145               150               155               160	
cgt ctc ggt cct tgg ggt ttc ttc aat ggg gtc gag ctc gcc aat gag	528
Arg Leu Gly Pro Trp Gly Phe Phe Asn Gly Val Glu Leu Ala Asn Glu	
165               170               175	
gga tcg tta aat ctc ggg ctg aag gac cag cgc ttg gcc ctg cat tgg	576
Gly Ser Leu Asn Leu Gly Leu Lys Asp Gln Arg Leu Ala Leu His Trp	
180               185               190	
gtg aaa gag aac att gca ggt ttc ggt ggc gac cct agt aaa gtc gtg	624
Val Lys Glu Asn Ile Ala Gly Phe Gly Gly Asp Pro Ser Lys Val Val	
195               200               205	
att tac gga caa agt gcc ggc tcc gaa agc gtg gga tac caa atc cgc	672
Ile Tyr Gly Gln Ser Ala Gly Ser Glu Ser Val Gly Tyr Gln Ile Arg	

## 21078W0.ST25.txt

210	215	220	
gcg tac aac ggc cga gat gac ggg ctc ttc cgc gga ggc atg atg gag			720
Ala Tyr Asn Gly Arg Asp Asp Gly Leu Phe Arg Gly Gly Met Met Glu			
225	230	235	240
tcc ggc gcg gtg tta cct ggc agt gcc ttg aac ctc acc tgg aca tat			768
Ser Gly Ala Val Leu Pro Gly Ser Ala Leu Asn Leu Thr Trp Thr Tyr			
245	250	255	
gag cct tgg ttc cag caa ata gca gac gag gca gga tgt tcc cag acc			816
Glu Pro Trp Phe Gln Gln Ile Ala Asp Glu Ala Gly Cys Ser Gln Thr			
260	265	270	
acc cgc aaa ctg gac tgt cta cgc cgc acg ccc ttc aca gtc cta aac			864
Thr Arg Lys Leu Asp Cys Leu Arg Arg Thr Pro Phe Thr Val Leu Asn			
275	280	285	
aac att ctg aac acc acc gcc aac gac acg cct tac aac tgg agg			912
Asn Ile Leu Asn Thr Thr Ala Asn Asp Thr Thr Pro Tyr Asn Trp Arg			
290	295	300	
ccc aca gtg gac ggt gac ttc gta gcg cga tat ccc agc gag caa ctc			960
Pro Thr Val Asp Gly Asp Phe Val Ala Arg Tyr Pro Ser Glu Gln Leu			
305	310	315	320
gac aca gga gac ttc gtc aaa gta cca atc ata atc ggc tac acc acg			1008
Asp Thr Gly Asp Phe Val Lys Val Pro Ile Ile Ile Gly Tyr Thr Thr			
325	330	335	
gac gaa gga aca aca gag tgc cca gaa cca gtg aac acc acc gcc gaa			1056
Asp Glu Gly Thr Thr Glu Cys Pro Glu Pro Val Asn Thr Thr Ala Glu			
340	345	350	
tta aaa gaa tac ctc agc tca aca aca acc tac ggc tgg gcc ctc gac			1104
Leu Lys Glu Tyr Leu Ser Ser Thr Thr Thr Tyr Gly Trp Ala Leu Asp			
355	360	365	
tca cag gta gta tcc tcg ctc ctg gac ctc tac ccc aac acc acc tcc			1152
Ser Gln Val Val Ser Ser Leu Leu Asp Leu Tyr Pro Asn Thr Thr Ser			
370	375	380	
ttc ggc atc cca tca tcc gaa gaa ctc ggc ggc aac gtc acc ttc cca			1200
Phe Gly Ile Pro Ser Ser Glu Glu Leu Gly Gly Asn Val Thr Phe Pro			
385	390	395	400
cag ccc tac ggc gcc gca ttc cgc cag acg gca gca tac tac ggc gac			1248
Gln Pro Tyr Gly Ala Ala Phe Arg Gln Thr Ala Ala Tyr Tyr Gly Asp			
405	410	415	
gcc cag ttc ata gcc gcg acg cgc tac acc tgt gag cta tgg gcg gca			1296
Ala Gln Phe Ile Ala Ala Thr Arg Tyr Thr Cys Glu Leu Trp Ala Ala			
420	425	430	
cat aac ctg aca gca tat tgc tac cga ttc aac acc aag aca gac gat			1344
His Asn Leu Thr Ala Tyr Cys Tyr Arg Phe Asn Thr Lys Thr Asp Asp			
435	440	445	
tac aac agg gaa gaa ggc gtg gcg cat ttc tcg gac gtg atc ttc atc			1392

## 21078WO.ST25.txt

Tyr Asn Arg Glu Glu Gly Val Ala His Phe Ser Asp Val Ile Phe Ile			
450	455	460	
ttc aac aac ctt aat ggt tat ggg ttc agt ccg aac ccg ttc acc aat			1440
Phe Asn Asn Leu Asn Gly Tyr Gly Phe Ser Pro Asn Pro Phe Thr Asn			
465	470	475	480
gct cca gag agc tat act gag ctt agc tac ctc atg tcc ggc tcg tgg			
Ala Pro Glu Ser Tyr Thr Glu Leu Ser Tyr Leu Met Ser Gly Ser Trp			
485	490	495	
atc agc ttc act aat agt ctg gat cct aat aag tgg act ggt cgc gga			1536
Ile Ser Phe Thr Asn Ser Leu Asp Pro Asn Lys Trp Thr Gly Arg Gly			
500	505	510	
agg aac gct acg aag acg gag aat tgg ccc gtg tat gat ctg gag aat			1584
Arg Asn Ala Thr Lys Thr Glu Asn Trp Pro Val Tyr Asp Leu Glu Asn			
515	520	525	
ccc ttg agt atg atc tgg gat gcg aat gtc act tcg tat gcg gcg ccg			1632
Pro Leu Ser Met Ile Trp Asp Ala Asn Val Thr Ser Tyr Ala Ala Pro			
530	535	540	
gat act tgg cgt aag gag ggt att gcg ttg att aat gct aat cgg agg			1680
Asp Thr Trp Arg Lys Glu Gly Ile Ala Leu Ile Asn Ala Asn Arg Arg			
545	550	555	560
gcg tat cag agg tga			
Ala Tyr Gln Arg			1695

&lt;210&gt; 33

&lt;211&gt; 564

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 33

Met Lys Gly Met Leu Pro Thr Leu Ser Trp Leu Ala Leu Gly Met Ala			
1	5	10	15
Ser Leu Ala Thr Cys Thr Asn Pro Val Ala Gln Thr Lys Asn Gly Ser			
20	25	30	
Tyr Tyr Gly Val Tyr Met Pro Gln Tyr Asn Glu Asp Tyr Phe Leu Gly			
35	40	45	
Ile Pro Phe Ala Lys Pro Pro Leu Ala His Leu Arg Trp Ala Asn Pro			
50	55	60	
Glu Ser Leu Asn Glu Ser Trp Ser Gly Leu Arg Pro Ala Thr Gly Tyr			
65	70	75	80
Ala Met Glu Cys Ile Gly Tyr Gly Ser Asp Gln Lys Gly Tyr Leu Gln			
85	90	95	
Ser Glu Asp Cys Leu Tyr Leu Asn Val Val Arg Pro Ala Glu Tyr Asp			
100	105	110	

## 21078WO.ST25.txt

Asn Ala Ser Leu Pro Val Leu Val Trp Ile His Gly Gly Gly Phe Ala  
           115                  120                  125  
 Gln Gly Gly Thr Pro Asp Leu Arg Tyr Asn Leu Thr Phe Ile Val Glu  
           130                  135                  140  
 His Ser Val Asn Ile Gly Gln Pro Ile Ile Ala Val Ser Val Ala Tyr  
           145                  150                  155                  160  
 Arg Leu Gly Pro Trp Gly Phe Phe Asn Gly Val Glu Leu Ala Asn Glu  
           165                  170                  175  
 Gly Ser Leu Asn Leu Gly Leu Lys Asp Gln Arg Leu Ala Leu His Trp  
           180                  185                  190  
 Val Lys Glu Asn Ile Ala Gly Phe Gly Gly Asp Pro Ser Lys Val Val  
           195                  200                  205  
 Ile Tyr Gly Gln Ser Ala Gly Ser Glu Ser Val Gly Tyr Gln Ile Arg  
           210                  215                  220  
 Ala Tyr Asn Gly Arg Asp Asp Gly Leu Phe Arg Gly Gly Met Met Glu  
           225                  230                  235                  240  
 Ser Gly Ala Val Leu Pro Gly Ser Ala Leu Asn Leu Thr Trp Thr Tyr  
           245                  250                  255  
 Glu Pro Trp Phe Gln Gln Ile Ala Asp Glu Ala Gly Cys Ser Gln Thr  
           260                  265                  270  
 Thr Arg Lys Leu Asp Cys Leu Arg Arg Thr Pro Phe Thr Val Leu Asn  
           275                  280                  285  
 Asn Ile Leu Asn Thr Thr Ala Asn Asp Thr Thr Pro Tyr Asn Trp Arg  
           290                  295                  300  
 Pro Thr Val Asp Gly Asp Phe Val Ala Arg Tyr Pro Ser Glu Gln Leu  
           305                  310                  315                  320  
 Asp Thr Gly Asp Phe Val Lys Val Pro Ile Ile Ile Gly Tyr Thr Thr  
           325                  330                  335  
 Asp Glu Gly Thr Thr Glu Cys Pro Glu Pro Val Asn Thr Thr Ala Glu  
           340                  345                  350  
 Leu Lys Glu Tyr Leu Ser Ser Thr Thr Thr Tyr Gly Trp Ala Leu Asp  
           355                  360                  365  
 Ser Gln Val Val Ser Ser Leu Leu Asp Leu Tyr Pro Asn Thr Thr Ser  
           370                  375                  380  
 Phe Gly Ile Pro Ser Ser Glu Glu Leu Gly Gly Asn Val Thr Phe Pro  
           385                  390                  395                  400  
 Gln Pro Tyr Gly Ala Ala Phe Arg Gln Thr Ala Ala Tyr Tyr Gly Asp  
           405                  410                  415  
 Ala Gln Phe Ile Ala Ala Thr Arg Tyr Thr Cys Glu Leu Trp Ala Ala  
           420                  425                  430  
 His Asn Leu Thr Ala Tyr Cys Tyr Arg Phe Asn Thr Lys Thr Asp Asp  
           435                  440                  445  
 Tyr Asn Arg Glu Glu Gly Val Ala His Phe Ser Asp Val Ile Phe Ile  
           450                  455                  460

## 21078W0.ST25.txt

Phe Asn Asn Leu Asn Gly Tyr Gly Phe Ser Pro Asn Pro Phe Thr Asn  
 465 470 475 480  
 Ala Pro Glu Ser Tyr Thr Glu Leu Ser Tyr Leu Met Ser Gly Ser Trp  
 485 490 495  
 Ile Ser Phe Thr Asn Ser Leu Asp Pro Asn Lys Trp Thr Gly Arg Gly  
 500 505 510  
 Arg Asn Ala Thr Lys Thr Glu Asn Trp Pro Val Tyr Asp Leu Glu Asn  
 515 520 525  
 Pro Leu Ser Met Ile Trp Asp Ala Asn Val Thr Ser Tyr Ala Ala Pro  
 530 535 540  
 Asp Thr Trp Arg Lys Glu Gly Ile Ala Leu Ile Asn Ala Asn Arg Arg  
 545 550 555 560  
 Ala Tyr Gln Arg

&lt;210&gt; 34

&lt;211&gt; 2371

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;400&gt; 34

gccctgacat ggacgggtgc agatagagac cgttggaaagg ctgaaccaca gggcacacgg	60
cacgttgagg accctgcatg ccgggtgtatc cggataatgg cagataatcc cggttaattg	120
ggggcgacgg cagctacggc tcacaaattt tgatggaaa gacacggcat gatgtttcaa	180
tgaagctcca aactttacag tgcttaggctg taaacgtgtataatcagc atgttaattga	240
ttatcatcta caactcaacc cccgcaccaa gaaatgaatc ctctcgtcgg aaaaaaaga	300
ccgcattcca gaagaacctt ttcctagata acaaacagta atcagtccat ccgtccctga	360
cgatcccccc atcgaacctc ggtaagacgc tcgacccaaa aaccagaccc acaagcttt	420
caacctccct aaacgaaaca acggctgtgt tgatcgtaa cgtggttgcc tataccaata	480
cgagaaccat ataggataga aattgagttt accgtggaaa agccacccgc tacagttaa	540
ttaaccaacc cacccacatg cccaaggcac ctgtAACAGG gactactgtc cagagagtgg	600
atagtggcta gtgggcagac gtcggatgaa ctccggaaa ccctaactga tacgtagaac	660
catcgtaac cctggttgtt ccctagttcg gggcgctatt cccagcgtag aaaagcgcc	720
gatcctctga aacagtttc ccccgggta tacttgctgtt ttagtcacta tcataaaaa	780
gtagtgttgtt ggacaagacc agggctact actattagtt agttctgttt catccgact	840
caattttgcg tcccaagacc ctgggttgc cgggcctgtc ttggccaaaca cgagatgtat	900
ggagtaagta tggagggaga ctaacctcg aatattctt tcttttttta gtactatcta	960
gcccttagtg agactatagc agtagtgaac cagagagaga gagagatgtc tatataagta	1020
cagtcgtaga tccctaaaca tgaccagctt cagactcaga ctcgagcagc cagtcgtac	1080
cagtccactc tttcattctc accccttctt tactatctt caataatttc tattcaataa	1140
gtctgcagtg cagcacccac acacattcat tctctgagag ataaaaaaa acaaaatggc	1200
ccccctcaaa tccctcctcc tcggccctc cctggccacc ctcgcccctt ccacccact	1260
ggcaaccgac gccgaaaacc tctaccacg tcaattcggc acgggctcta cagccaacga	1320
actcgagcag ggaagctgca aggatgtgac tctcatctt gcgaggggtt caactgagct	1380

## 21078WO.ST25.txt

tggaaatatg	gtatgcttgt	tgcctgcctt	tacccgtact	atactatccc	agaacatacc	1440
aagcacaca	tcacaaaaca	tgtggagcca	ggagcta	agtgggtgt	atgatatgt	1500
gtagggcacc	gtaatcg	cccctctcg	cgacaac	aaatccaaac	tcggatccga	1560
caaagtgc	tgccagg	tcggcgcca	atacagc	ggactcgtgc	agaatgcc	1620
gccccaga	accgatcc	ggagtatctc	cgcgcga	cagatgttc	aggaggcgaa	1680
ttcgaagt	cccaata	agattgtgc	gggtgg	aggtatata	cccttccc	1740
tttacctt	cccatatcaa	tgctagaggc	aaaggaat	catgcta	tagatgttgg	1800
ggaaacag	aaggaagc	tgtgattgac	aacgc	aagaactc	caccacc	1860
aaagacca	taaagggt	cgtgcttc	gggttca	gaaacgt	ggatcac	1920
cagatcc	attaccctaa	gatgacgt	agg	gttcc	cgatctgg	1980
tgtgatg	cg	ttgtgtt	ttgttgc	atgttgc	tgccgttgc	2040
gcggcg	gagct	tttggcc	gaagg	tttcc	tttcc	2100
tcggatg	ccg	cgatgtt	tttgc	tttgc	tttgc	2160
tcttctt	ttt	ttggagg	tttgc	tttgc	tttgc	2220
tttaggg	tttgc	tttgc	tttgc	tttgc	tttgc	2280
ataagatata	tgttacatag	tatagatgt	ttgttgc	tttgc	tttgc	2340
tttgacatga	tctgc	atata	gggagcgt	tttgc	tttgc	2371

&lt;210&gt; 35

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(789)

&lt;400&gt; 35

atg	gcc	ccc	ctc	aaa	tcc	ctc	ctc	ggc	gcc	tcc	ctg	gcc	acc	ctc	48
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Met	Ala	Pro	Leu	Lys	Ser	Leu	Leu	Leu	Gly	Ala	Ser	Leu	Ala	Thr	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1	5	10	15
---	---	----	----

gcc	ctt	tcc	acc	cca	ctg	gca	acc	gac	gcc	gaa	aac	ctc	tac	gca	cgt	96
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Ala	Leu	Ser	Thr	Pro	Leu	Ala	Thr	Asp	Ala	Glu	Asn	Leu	Tyr	Ala	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20	25	30
----	----	----

caa	ttc	ggc	acg	ggc	tct	aca	gcc	aac	gaa	ctc	gag	cag	gga	agc	tgc	144
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Gln	Phe	Gly	Thr	Gly	Ser	Thr	Ala	Asn	Glu	Leu	Glu	Gln	Gly	Ser	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
----	----	----

aag	gat	gtg	act	ctc	atc	ttt	g	agg	ggg	tca	act	gag	ctt	ggg	aat	192
-----	-----	-----	-----	-----	-----	-----	---	-----	-----	-----	-----	-----	-----	-----	-----	-----

Lys	Asp	Val	Thr	Leu	Ile	Phe	Ala	Arg	Gly	Ser	Thr	Glu	Leu	Gly	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
----	----	----

atg	ggc	acc	gta	atc	ggc	ccc	cct	ctc	tgc	gac	aac	ctg	aaa	tcc	aaa	240
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Met	Gly	Thr	Val	Ile	Gly	Pro	Pro	Leu	Cys	Asp	Asn	Leu	Lys	Ser	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65	70	75	80
----	----	----	----

## 21078WO.ST25.txt

ctc gga tcc gac aaa gtc gcc tgc cag ggt gtc ggc ggc caa tac agc Leu Gly Ser Asp Lys Val Ala Cys Gln Gly Val Gly Gln Tyr Ser	288
85 90 95	
gcc gga ctc gtg cag aat gcc ctg ccc cag aac acc gat ccg ggg agt Ala Gly Leu Val Gln Asn Ala Leu Pro Gln Asn Thr Asp Pro Gly Ser	336
100 105 110	
atc tcc gcc gcg aag cag atg ttc gag gag gcg aat tcg aag tgt ccc Ile Ser Ala Ala Lys Gln Met Phe Glu Glu Ala Asn Ser Lys Cys Pro	384
115 120 125	
aat act aag att gtt gcg ggt ggt tat agt caa gga agc gct gtg att Asn Thr Lys Ile Val Ala Gly Gly Tyr Ser Gln Gly Ser Ala Val Ile	432
130 135 140	
gac aac gcc gtg caa gaa ctc agc acc acc gtg aaa gac caa gtg aag Asp Asn Ala Val Gln Glu Leu Ser Thr Thr Val Lys Asp Gln Val Lys	480
145 150 155 160	
ggt gtc gtg ctc ttc ggg ttc acg aga aac gtg cag gat cac ggg cag Gly Val Val Leu Phe Gly Phe Thr Arg Asn Val Gln Asp His Gly Gln	528
165 170 175	
atc cct aat tac cct aag gat gac gtg aag gtt tat tgt gcc gtg ggc Ile Pro Asn Tyr Pro Lys Asp Asp Val Lys Val Tyr Cys Ala Val Gly	576
180 185 190	
gat ctg gtc tgt gat gat acg ttg gtt acg gcg atg cat ctg acg Asp Leu Val Cys Asp Asp Thr Leu Val Val Thr Ala Met His Leu Thr	624
195 200 205	
tat ggc atg gat gcg ggt gat gcg gcg agc ttt ttg gcc gag aag gtg Tyr Gly Met Asp Ala Gly Asp Ala Ala Ser Phe Leu Ala Glu Lys Val	672
210 215 220	
cag tct tcc agt agt tcg act act agc tcc agc tcg gat gcc gcg agt Gln Ser Ser Ser Ser Thr Thr Ser Ser Ser Asp Ala Ala Ser	720
225 230 235 240	
agt tca tct gct gcg ggg acg tcg tcg tcg ggg ttg tcg gga ctg tct Ser Ser Ser Ala Ala Gly Thr Ser Ser Ser Gly Leu Ser Gly Leu Ser	768
245 250 255	
tct ttt ttt gga ggt ctc taa Ser Phe Phe Gly Gly Leu	789
260	

&lt;210&gt; 36

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 36

## 21078WO.ST25.txt

Met Ala Pro Leu Lys Ser Leu Leu Leu Gly Ala Ser Leu Ala Thr Leu  
 1 5 10 15  
 Ala Leu Ser Thr Pro Leu Ala Thr Asp Ala Glu Asn Leu Tyr Ala Arg  
 20 25 30  
 Gln Phe Gly Thr Gly Ser Thr Ala Asn Glu Leu Glu Gln Gly Ser Cys  
 35 40 45  
 Lys Asp Val Thr Leu Ile Phe Ala Arg Gly Ser Thr Glu Leu Gly Asn  
 50 55 60  
 Met Gly Thr Val Ile Gly Pro Pro Leu Cys Asp Asn Leu Lys Ser Lys  
 65 70 75 80  
 Leu Gly Ser Asp Lys Val Ala Cys Gln Gly Val Gly Gln Tyr Ser  
 85 90 95  
 Ala Gly Leu Val Gln Asn Ala Leu Pro Gln Asn Thr Asp Pro Gly Ser  
 100 105 110  
 Ile Ser Ala Ala Lys Gln Met Phe Glu Glu Ala Asn Ser Lys Cys Pro  
 115 120 125  
 Asn Thr Lys Ile Val Ala Gly Gly Tyr Ser Gln Gly Ser Ala Val Ile  
 130 135 140  
 Asp Asn Ala Val Gln Glu Leu Ser Thr Thr Val Lys Asp Gln Val Lys  
 145 150 155 160  
 Gly Val Val Leu Phe Gly Phe Thr Arg Asn Val Gln Asp His Gly Gln  
 165 170 175  
 Ile Pro Asn Tyr Pro Lys Asp Asp Val Lys Val Tyr Cys Ala Val Gly  
 180 185 190  
 Asp Leu Val Cys Asp Asp Thr Leu Val Val Thr Ala Met His Leu Thr  
 195 200 205  
 Tyr Gly Met Asp Ala Gly Asp Ala Ala Ser Phe Leu Ala Glu Lys Val  
 210 215 220  
 Gln Ser Ser Ser Ser Thr Thr Ser Ser Ser Asp Ala Ala Ser  
 225 230 235 240  
 Ser Ser Ser Ala Ala Gly Thr Ser Ser Ser Gly Leu Ser Gly Leu Ser  
 245 250 255  
 Ser Phe Phe Gly Gly Leu  
 260

<210> 37  
 <211> 2981  
 <212> DNA  
 <213> Aspergillus niger

<400> 37  
 tcctcatccc atgctctccc ggcagaaccc cggagacaac ccacactaat gcacccaaag 60  
 caaaaatgaca tggattgaat tatccgggtt gcatccatct tgtccccca cacattggac 120

## 21078W0.ST25.txt

ccttcctta	taatggctgc	ccggcaa	acccccaa	tgtttaggcc	agcgca	gata	180
gcaa	atctct	cgtctgatta	acgatgctaa	agctcgctgt	tgctctttt	tcgttacttg	240
ccgtggcaa	tgca	gccc	acc	ggc	cagt	cct	300
ttcgcaacgg	tacat	atgc	ccag	caag	at	ttttgg	360
aatgcc	tgcc	cagc	ctttaggt	acttgc	cacgg	tcct	420
acgaaagctg	gagt	ggcg	aggaa	atattc	caat	atctgt	480
gtgtgagtgc	gcaa	atcttc	ttcg	agag	cc	ggc	540
aatataatct	aatgg	gtaga	tctgtt	actcg	att	ggta	600
ttgtctaacc	ttga	atgtca	tccgcattc	ttctgc	aaat	gagaact	660
ggcg	ctgg	at	aca	gat	ggat	ctgt	720
catgtcccg	attgtt	gcca	actc	cata	aa	gttgt	780
attagactg	ctcg	gcttgc	tcgc	atttgc	g	gat	840
tatcgcc	tt	cgcatggg	cttctt	gag	tc	ggcac	900
aatctagg	ta	ca	agg	tttgc	ca	aggagaa	960
ttcggagg	agg	acc	ca	actatc	ttgg	ccgg	1020
ggttatc	acc	ttc	ttc	actatc	ggc	gtgtcc	1080
gagtcagg	gg	actatt	gc	acttcc	cc	gcactat	1140
gatgagct	cg	ggta	cg	ttgc	tc	gtgtcc	1200
gaagttcc	gt	gaaaatt	ga	acgt	ct	tcggat	1260
aatttcgg	cc	gtt	ca	acac	cc	gtt	1320
aagcatga	at	tcgt	aa	ccattt	tttgc	atacc	1380
tttggccc	c	agg	tat	tttgc	tttgc	aggacag	1440
gataat	tg	aaat	ttc	tttgc	tttgc	tttgc	1500
agatgg	tc	tttgc	tttgc	tttgc	tttgc	tttgc	1560
ccctgat	cc	agg	tttgc	tttgc	tttgc	tttgc	1620
aggctac	aa	tttgc	tttgc	tttgc	tttgc	tttgc	1680
tcgccc	tt	tttgc	tttgc	tttgc	tttgc	tttgc	1740
tatgc	tt	tttgc	tttgc	tttgc	tttgc	tttgc	1800
tgtattca	aa	tttgc	tttgc	tttgc	tttgc	tttgc	1860
cgagt	tt	tttgc	tttgc	tttgc	tttgc	tttgc	1920
tttagacc	tt	tttgc	tttgc	tttgc	tttgc	tttgc	1980
tcagcc	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2040
tttagacc	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2100
agctt	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2160
ttgc	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2220
agtc	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2280
tcct	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2340
tccg	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2400
agcatt	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2460
tttag	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2520
acagc	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2580
atgtac	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2640
ccaag	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2700
caaga	tt	tttgc	tttgc	tttgc	tttgc	tttgc	2760

## 21078WO.ST25.txt

taaccaagtc cccgattgt	ctacggctac caaaactaga atgatgaaaa tattggagta	2820
cgaaaggaac taaaccaata ctaagaaaaa aaaaaaagag taaagaaaaa agagtaaaa		2880
accaagctcg gaaagtaaaa atttcccctg gtcttgtt cattcccta cctattgaga		2940
accgggttca ccaatgacag cgatccccg atttgacatc g		2981

<210> 38  
<211> 1686  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> CDS  
<222> (1)..(1686)

<400> 38		
atg cta aag ctc gct gtt ctt ttt tcg tta ctt gcc gtg ggc aat		48
Met Leu Lys Leu Ala Val Ala Leu Phe Ser Leu Leu Ala Val Gly Asn		
1 5 10 15		
gca gcg cca acc aaa gtg gcc cgt tcc acg gcc agt cct acg gcc aag		96
Ala Ala Pro Thr Lys Val Ala Arg Ser Thr Ala Ser Pro Thr Ala Lys		
20 25 30		
gtt cgc aac ggt aca tat gtc gga gtg aca aat gcg cat tac cag caa		144
Val Arg Asn Gly Thr Tyr Val Gly Val Thr Asn Ala His Tyr Gln Gln		
35 40 45		
gat ttc ttt ttg gga atg ccg tat gcc cag cag cct tta ggt gac ttg		192
Asp Phe Phe Leu Gly Met Pro Tyr Ala Gln Gln Pro Leu Gly Asp Leu		
50 55 60		
cgc ttc acg gtg cct cag tcc ctg aac gaa agc tgg agt ggc gag cgc		240
Arg Phe Thr Val Pro Gln Ser Leu Asn Glu Ser Trp Ser Gly Glu Arg		
65 70 75 80		
gac gcg aag gaa tat tcc aat atc tgt gta gga tac ggt acc gac tcg		288
Asp Ala Lys Glu Tyr Ser Asn Ile Cys Val Gly Tyr Gly Thr Asp Ser		
85 90 95		
att tgg tac cca cag tcc gaa gct tgt cta acc ttg aat gtc atc cgc		336
Ile Trp Tyr Pro Gln Ser Glu Ala Cys Leu Thr Leu Asn Val Ile Arg		
100 105 110		
gat tct tct gca aat gag aac tcg aag ctc ccc gtg ggc gtc tgg ata		384
Asp Ser Ser Ala Asn Glu Asn Ser Lys Leu Pro Val Gly Val Trp Ile		
115 120 125		
cat gga ggt ggc ttc ttt gag gga tct agt gct gac cag cgc tac aac		432
His Gly Gly Phe Phe Glu Gly Ser Ser Ala Asp Gln Arg Tyr Asn		
130 135 140		
atg tcc gcg att gtt gcc aac tcc tat aag atc gga aag ccg ttc att		480

## 21078WO.ST25.txt

Met Ser Ala Ile Val Ala Asn Ser Tyr Lys Ile Gly Lys Pro Phe Ile			
145	150	155	160
gct gtc agc tta aac tat cgc ctt tcg gca tgg ggc ttc ttg agt tcc			528
Ala Val Ser Leu Asn Tyr Arg Leu Ser Ala Trp Gly Phe Leu Ser Ser			
165	170	175	
agt caa gtc tgg ggc act ggc aat acc aat cta ggt atc agg gat caa			576
Ser Gln Val Trp Gly Thr Gly Asn Thr Asn Leu Gly Ile Arg Asp Gln			
180	185	190	
agg tta gca ctc cat tgg atc aag gag aat atc gcg gca ttc gga gga			624
Arg Leu Ala Leu His Trp Ile Lys Glu Asn Ile Ala Ala Phe Gly Gly			
195	200	205	
gac cca gat aag atc act atc tgg ggc gaa tct gcc gga gcg atg tcc			672
Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser Ala Gly Ala Met Ser			
210	215	220	
gtg ggt tat cac ctt gca gca tac ggc ggt agg gac gat gga ctc ttc			720
Val Gly Tyr His Leu Ala Ala Tyr Gly Gly Arg Asp Asp Gly Leu Phe			
225	230	235	240
cgt gga gga att atg gag tca gga ggg act att gca gct agt cca gcc			768
Arg Gly Gly Ile Met Glu Ser Gly Gly Thr Ile Ala Ala Ser Pro Ala			
245	250	255	
aac tat acc ggg tac caa gcg cac tat gat gag ctc gcg ggt caa gtc			816
Asn Tyr Thr Gly Tyr Gln Ala His Tyr Asp Glu Leu Ala Gly Gln Val			
260	265	270	
ggt tgc tcc gac gta gta gat tcg ttg cag tgc ctg cgc gaa gtt ccg			864
Gly Cys Ser Asp Val Val Asp Ser Leu Gln Cys Leu Arg Glu Val Pro			
275	280	285	
ttc gag aaa ttg aac gct gct ctc aac acc acc agt ggt aac tcg gat			912
Phe Glu Lys Leu Asn Ala Ala Leu Asn Thr Thr Ser Gly Asn Ser Asp			
290	295	300	
ttc aat ttc ggg ccc gtc att gat gga gat ata atc agg gac tgg ggc			960
Phe Asn Phe Gly Pro Val Ile Asp Gly Asp Ile Ile Arg Asp Trp Gly			
305	310	315	320
agc ctc cag cta gac aag cat gaa ttc gtc aaa gtc cct att ctt gca			1008
Ser Leu Gln Leu Asp Lys His Glu Phe Val Lys Val Pro Ile Leu Ala			
325	330	335	
ggt acc aat acc gac gaa ggg aca gcc ttt ggg ccc aca ggt atc aac			1056
Gly Thr Asn Thr Asp Glu Gly Thr Ala Phe Gly Pro Thr Gly Ile Asn			
340	345	350	
acg aca gag gag ttc tat gca tat ctc aca gat ggc gaa tct gga ttc			1104
Thr Thr Glu Glu Phe Tyr Ala Tyr Leu Thr Asp Gly Glu Ser Gly Phe			
355	360	365	
cag cta ccc ccc acg atc gcc cag gaa atc ctg cag ctc tac cct gat			1152
Gln Leu Pro Pro Thr Ile Ala Gln Glu Ile Leu Gln Leu Tyr Pro Asp			
370	375	380	

## 21078WO.ST25.txt

gat cca gca ctg ggc atc ccc gaa ttt ctc ggt gac act aga gtc ccg Asp Pro Ala Leu Gly Ile Pro Glu Phe Leu Gly Asp Thr Arg Val Pro 385 390 . 395 400	1200
tcc aaa ggc tac caa tgg cg <sup>c</sup> acc tgt gca tac gca ggg gac tat Ser Lys Gly Tyr Gln Trp Arg Arg Thr Cys Ala Tyr Ala Gly Asp Tyr 405 410 415	1248
gta atg cat gcc aac cgt cgc cga caa tgt gag gc <sup>g</sup> tgg aca gag acc Val Met His Ala Asn Arg Arg Gln Cys Glu Ala Trp Thr Glu Thr 420 425 430	1296
tcg acg acg gc <sup>g</sup> tac tgt tat cga ttc aat atg cgt gc <sup>g</sup> gcc gat gtc Ser Thr Thr Ala Tyr Cys Tyr Arg Phe Asn Met Arg Ala Ala Asp Val 435 440 445	1344
ccc atc ctg tct ggc acc cat ttt gaa gaa gtt gct ttt gta ttc Pro Ile Leu Ser Gly Ala Thr His Phe Glu Glu Val Ala Phe Val Phe 450 455 460	1392
aac aac att gca gga ctc ggg tac cat tac gga aag cc <sup>g</sup> ttc gca ggg Asn Asn Ile Ala Gly Leu Gly Tyr His Tyr Gly Lys Pro Phe Ala Gly 465 470 475 480	1440
atg ccc gag tcc tac gta cag cta agc aac ttg atg acc agc atg tgg Met Pro Glu Ser Tyr Val Gln Leu Ser Asn Leu Met Thr Ser Met Trp 485 490 495	1488
gca tcc ttc atc cac gat tta gac cct aat tcg ggc atc aag gac tca Ala Ser Phe Ile His Asp Leu Asp Pro Asn Ser Gly Ile Lys Asp Ser 500 505 510	1536
gct gta cag tgg caa ccg tac ggg aag gat cag cc <sup>g</sup> gtt gat cta gtg Ala Val Gln Trp Gln Pro Tyr Gly Lys Asp Gln Pro Val Asp Leu Val 515 520 525	1584
ttt gat gc <sup>g</sup> aat gtc acg agc tac agc tac atg gag cca gac acg tgg Phe Asp Ala Asn Val Thr Ser Tyr Ser Tyr Met Glu Pro Asp Thr Trp 530 535 540	1632
cg <sup>g</sup> aag gag ggg atc gac tat atc aat tcc gtg gc <sup>g</sup> aac gc <sup>g</sup> tac tgg Arg Lys Glu Gly Ile Asp Tyr Ile Asn Ser Val Ala Asn Ala Tyr Trp 545 550 555 560	1680
cga taa Arg	1686

&lt;210&gt; 39

&lt;211&gt; 561

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 39

Met Leu Lys Leu Ala Val Ala Leu Phe Ser Leu Leu Ala Val Gly Asn

## 21078WO.ST25.txt

1	5	10	15
Ala	Ala	Pro	Thr
Lys	Val	Ala	Arg
Ser	Thr	Ala	Ser
Pro	Thr	Ala	Lys
20	25	30	
Val	Arg	Asn	Gly
Gly	Thr	Tyr	Val
Val	Gly	Val	Thr
Asn	Ala	His	Tyr
Gln	Gln		
35	40	45	
Asp	Phe	Phe	Leu
Gly	Met	Pro	Tyr
Ala	Gln	Gln	Pro
Leu	Gly	Asp	Leu
50	55	60	
Arg	Phe	Thr	Val
Pro	Gln	Ser	Leu
Asn	Glu	Ser	Trp
Gly	Glu	Trp	Ser
Arg			
65	70	75	80
Asp	Ala	Lys	Glu
Tyr	Ser	Asn	Ile
Cys	Val	Gly	Tyr
Gly	Tyr	Gly	Thr
Thr	Asp	Ser	
Ile	Trp	Tyr	Pro
Gln	Ser	Glu	Ala
Cys	Leu	Thr	Leu
Asn	Val	Asn	Val
Val	Ile	Arg	
100	105	110	
Asp	Ser	Ser	Ala
Ala	Asn	Glu	Asn
Ser	Lys	Leu	Pro
Val	Gly	Val	Trp
Gly	Val	Ile	
115	120	125	
His	Gly	Gly	Phe
Gly	Gly	Phe	Glu
Gly	Ser	Ser	Ala
Asp	Gln	Arg	Tyr
130	135	140	Asn
Met	Ser	Ala	Ile
Ile	Val	Ala	Asn
Ser	Tyr	Lys	Ile
Gly	Lys	Pro	Phe
145	150	155	Ile
Ala	Val	Ser	Leu
Asn	Tyr	Arg	Leu
Ser	Ala	Trp	Gly
Phe	Leu	Ser	Ser
165	170	175	
Ser	Gln	Val	Trp
Gly	Thr	Gly	Asn
Asn	Leu	Gly	Ile
Arg	Ile	Arg	Asp
180	185	190	Gln
Arg	Leu	Ala	Leu
His	Trp	Ile	Lys
Glu	Asn	Ile	Ala
Ala	Phe	Gly	Gly
195	200	205	
Asp	Pro	Asp	Lys
Ile	Thr	Ile	Trp
Gly	Glu	Ser	Ala
Gly	Ala	Met	Ser
210	215	220	
Val	Gly	Tyr	His
His	Leu	Ala	Ala
Tyr	Gly	Gly	Arg
Arg	Asp	Asp	Gly
225	230	235	Leu
Phe	Gly	Ile	Phe
Met	Glu	Ser	Gly
Gly	Thr	Ile	Ala
Ala	Ala	Ser	Pro
240			Ala
Asn	Tyr	Thr	Gly
Gly	Tyr	Gln	Ala
Ala	His	Tyr	Asp
Glu	Leu	Ala	Gly
260	265	270	Gln
Val	Gly	Ser	Val
Cys	Ser	Asp	Val
275	280	285	Asp
Phe	Glu	Lys	Leu
Leu	Asn	Ala	Ala
Asn	Ala	Leu	Asn
290	295	300	Thr
Thr	Thr	Ser	Gly
Gly	Asn	Asp	Gly
305	310	315	Asp
Phe	Asn	Phe	Gly
Gly	Pro	Val	Ile
320			Asp
Ser	Leu	Gln	Leu
Leu	Asp	Lys	Asn
Asp	His	Glu	Phe
Gly	Thr	Val	Gly
Ala	Phe	Gly	Pro
335	330	335	Thr
Gly	Thr	Asn	Asp
Asp	Glu	Gly	Gly
340	345	350	Thr
Thr	Thr	Glu	Gly
Glu	Gly	Asp	Gly
Asp	Gly	Glu	Phe
Thr	Thr	Gly	

## 21078WO.ST25.txt

355                   360                   365  
Gln Leu Pro Pro Thr Ile Ala Gln Glu Ile Leu Gln Leu Tyr Pro Asp  
370                   375                   380  
Asp Pro Ala Leu Gly Ile Pro Glu Phe Leu Gly Asp Thr Arg Val Pro  
385                   390                   395                   400  
Ser Lys Gly Tyr Gln Trp Arg Arg Thr Cys Ala Tyr Ala Gly Asp Tyr  
405                   410                   415  
Val Met His Ala Asn Arg Arg Gln Cys Glu Ala Trp Thr Glu Thr  
420                   425                   430  
Ser Thr Thr Ala Tyr Cys Tyr Arg Phe Asn Met Arg Ala Ala Asp Val  
435                   440                   445  
Pro Ile Leu Ser Gly Ala Thr His Phe Glu Glu Val Ala Phe Val Phe  
450                   455                   460  
Asn Asn Ile Ala Gly Leu Gly Tyr His Tyr Gly Lys Pro Phe Ala Gly  
465                   470                   475                   480  
Met Pro Glu Ser Tyr Val Gln Leu Ser Asn Leu Met Thr Ser Met Trp  
485                   490                   495  
Ala Ser Phe Ile His Asp Leu Asp Pro Asn Ser Gly Ile Lys Asp Ser  
500                   505                   510  
Ala Val Gln Trp Gln Pro Tyr Gly Lys Asp Gln Pro Val Asp Leu Val  
515                   520                   525  
Phe Asp Ala Asn Val Thr Ser Tyr Ser Tyr Met Glu Pro Asp Thr Trp  
530                   535                   540  
Arg Lys Glu Gly Ile Asp Tyr Ile Asn Ser Val Ala Asn Ala Tyr Trp  
545                   550                   555                   560  
Arg